# Figure 1A

#### 4.1.1 Heavy Chain DNA

```
ATGGAGTTTG GGCTGAGCTG GGTTTTCCTC GTTGCTCTTT TAAGAGGTGT 50
CCAGTGTCAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCCAGCCTG 100
GGAGGTCCCT GAGACTCTCC TGTGTAGCGT CTGGATTCAC CTTCAGTAGC 150
CATGCCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT 200
GGCAGTTATA TGGTATGATG GAAGAAATAA ATACTATGCA GACTCCGTGA 250
AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC GCTGTTTCTG 300
CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ACTGTGCGAG 350
AGGAGGTCAC TTCGGTCCTT TTGACTACTG GGGCCAGGGA ACCCTGGTCA 400
CCGTCTCCTC AGCCTCCACC AAGGGCCCAT CGGTCTTCCC CCTGGCGCCC 450
TGCTCCAGGA GCACCTCCGA GAGCACAGCG GCCCTGGGCT GCCTGGTCAA 500
GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCTCTGA 550
CCAGCGGCGT GCACACCTTC CCAGCTGTCC TACAGTCCTC AGGACTCTAC 600
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAACTTCG GCACCCAGAC 650
CTACACCTGC AACGTAGATC ACAAGCCCAG CAACACCAAG GTGGACAAGA 700
CAGTTGAGCG CAAATGTTGT GTCGAGTGCC CACCGTGCCC AGCACCACCT 750
GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CCAAAACCCA AGGACACCCT 800
CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC 850
ACGAAGACCC CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG 900
CATAATGCCA AGACAAAGCC ACGGGAGGAG CAGTTCAACA GCACGTTCCG 950
TGTGGTCAGC GTCCTCACCG TTGTGCACCA GGACTGGCTG AACGGCAAGG 1000
AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCCAGCCCC CATCGAGAAA 1050
ACCATCTCCA AAACCAAAGG GCAGCCCCGA GAACCACAGG TGTACACCCT 1100
GCCCCATCC CGGGAGGAGA TGACCAAGAA CCAGGTCAGC CTGACCTGCC 1150
TGGTCAAAGG CTTCTACCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT 1200
GGGCAGCCGG AGAACAACTA CAAGACCACA CCTCCCATGC TGGACTCCGA 1250
CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC 1300
AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC 1350
CACTACACGC AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GA
```

(SEQ ID NO:27)

#### 4.1.1 Heavy Chain Protein

```
MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCVASGFTFSS50HGMHWVRQAPGKGLEWVAVIWYDGRNKYYADSVKGRFTISRDNSKNTLFL100QMNSLRAEDTAVYYCARGGHFGPFDYWGQGTLVTVSSASTKGPSVFPLAP150CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY200SLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPP250VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV300HNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEK350TISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN400GQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN450HYTQKSLSLSPGK463
```

(SEQ ID NO:1)

# Figure 1A (continued)

#### 4.1.1 Kappa Chain DNA

```
ATGGAAACCC CAGCGCAGCT TCTCTTCCTC CTGCTACTCT GGCTCCCAGA 50
TACCACCGGA GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT 100
CTCCAGGGGA AAGAGCCACC CTCTCCTGCA GGGCCAGTCA GAGTATTAGC 150
AGCAGCTTCT TAGCCTGGTA CCAGCAGAGA CCTGGCCAGG CTCCCAGGCT 200
CCTCATCTAT GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA 250
GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG 300
CCTGAAGATT TTGCAGTGTA TTACTGTCAG CAGTATGGTA CCTCACCCTG 350
GACGTTCGGC CAAGGGACCA AGGTGGAAAT CAAACGAACT GTGGCTGCAC 400
CATCTGTCTT CATCTTCCCG CCATCTGATG AGCAGTTGAA ATCTGGAACT 450
GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT 500
ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG 550
TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG 600
ACGCTGAGCA AAGCAGCACA CAGAGCACCT ACAGCCTCAG CAGCACCCTG 600
ACGCTGAGCA GACCAGCACA CAGAGCACCT ACAGCCTCAG CCTGCGAAGT 650
CACCCATCAG GGCCTGAGCT CGCCCGTCAC AAAGGCCTC AACAGGGGAG 700
AGTGTTAG
```

(SEQ ID NO:40)

#### 4.1.1 Kappa Chain Protein

| METPAQLLFL | LLLWLPDTTG | EIVLTQSPGT | LSLSPGERAT | LSCRASQSIS | 50  |
|------------|------------|------------|------------|------------|-----|
|            |            |            |            | DFTLTISRLE |     |
| PEDFAVYYCQ | QYGTSPWTFG | QGTKVE1KRT | VAAPSVFIFP | PSDEQLKSGT | 150 |
| ASVVCLLNNF | YPREAKVQWK | VDNALQSGNS | QESVTEQDSK | DSTYSLSSTL | 200 |
| TLSKADYEKH | KVYACEVTHQ | GLSSPVTKSF | NRGEC      |            | 235 |

(SEQ ID NO:14)

# Figure 1B

# 4.8.1 Heavy Chain DNA

| ATGGAGTTTG | GGCTGAGCTG | GGTTTTCCTC | GTTGCTCTTT | TAAGAGGTGT | 50   |
|------------|------------|------------|------------|------------|------|
| CCAGTGTCAG | GTGCAGCTGG | TGGAGTCTGG | GGGAGGCGTG | GTCCAGCCTG | 100  |
| GGAGGTCCCT | GAGACTCTCC | TGTACAGCGT | CTGGATTCAC | CTTCAGTAAC | 150  |
| TATGGCATGC | ACTGGGTCCG | CCAGGCTCCA | GGCAAGGGGC | TGGAGTGGGT | 200  |
| GGCAGTTATA | TGGTATGATG | GAAGTAATAA | ACACTATGGA | GACTCCGTGA | 250  |
| AGGGCCGATT | CACCATCTCC | AGTGACAATT | CCAAGAACAC | GCTGTATCTG | 300  |
| CAAATGAACA | GCCTGAGAGC | CGAGGACACG | GCTGTGTATT | ACTGTGCGAG | 350  |
| AGGAGAGA   | CTGGGGTCCT | ACTTTGACTA | CTGGGGCCAG | GGAACCCTGG | 400  |
| TCACCGTCTC | CTCAGCCTCC | ACCAAGGGCC | CATCGGTCTT | CCCCTGGCG  | 450  |
| CCCTGCTCCA | GGAGCACCTC | CGAGAGCACA | GCGGCCCTGG | GCTGCCTGGT | 500  |
| CAAGGACTAC | TTCCCCGAAC | CGGTGACGGT | GTCGTGGAAC | TCAGGCGCTC | 550  |
| TGACCAGCGG | CGTGCACACC | TTCCCAGCTG | TCCTACAGTC | CTCAGGACTC | 600  |
| TACTCCCTCA | GCAGCGTGGT | GACCGTGCCC | TCCAGCAACT | TCGGCACCCA | 650  |
| GACCTACACC | TGCAACGTAG | ATCACAAGCC | CAGCAACACC | AAGGTGGACA | 700  |
| AGACAGTTGA | GCGCAAATGT | TGTGTCGAGT | GCCCACCGTG | CCCAGCACCA | 750  |
| CCTGTGGCAG | GACCGTCAGT | CTTCCTCTTC | CCCCCAAAAC | CCAAGGACAC | 800  |
| CCTCATGATC | TCCCGGACCC | CTGAGGTCAC | GTGCGTGGTG | GTGGACGTGA | 850  |
| GCCACGAAGA | CCCCGAGGTC | CAGTTCAACT | GGTACGTGGA | CGGCGTGGAG | 900  |
| GTGCATAATG | CCAAGACAAA | GCCACGGGAG | GAGCAGTTCA | ACAGCACGTT | 950  |
| CCGTGTGGTC | AGCGTCCTCA | CCGTTGTGCA | CCAGGACTGG | CTGAACGGCA | 1000 |
| AGGAGTACAA | GTGCAAGGTC | TCCAACAAAG | GCCTCCCAGC | CCCCATCGAG | 1050 |
| AAAACCATCT |            | AGGGCAGCCC |            |            | 1100 |
| CCTGCCCCCA | TCCCGGGAGG | AGATGACCAA | GAACCAGGTC | AGCCTGACCT | 1150 |
| GCCTGGTCAA | AGGCTTCTAC | CCCAGCGACA | TCGCCGTGGA | GTGGGAGAGC | 1200 |
| AATGGGCAGC | CGGAGAACAA | CTACAAGACC |            |            | 1250 |
| CGACGGCTCC | TTCTTCCTCT | ACAGCAAGCT | CACCGTGGAC | AAGAGCAGGT | 1300 |
| GGCAGCAGGG | GAACGTCTTC | TCATGCTCCG | TGATGCATGA | GGCTCTGCAC | 1350 |
| AACCACTACA | CGCAGAAGAG | CCTCTCCCTG | TCTCCGGGTA | AATGA      | 1395 |

(SEQ ID NO:28)

# 4.8.1 Heavy Chain Protein

| MEFGLSWVFL | VALLRGVQCQ | VQLVESGGGV | VQPGRSLRLS | CTASGFTFSN        | 50 - |
|------------|------------|------------|------------|-------------------|------|
| YGMHWVRQAP | GKGLEWVAVI | WYDGSNKHYG | DSVKGRFTIS | SDNSKNTLYL        | 100  |
| QMNSLRAEDT | AVYYCARGER | LGSYFDYWGQ | GTLVTVSSAS | TKGPSVFPLA        | 150  |
| PCSRSTSEST | AALGCLVKDY | FPEPVTVSWN | SGALTSGVHT | FPAVLQSSGL        | 200  |
| YSLSSVVTVP | SSNFGTQTYT | CNVDHKPSNT | KVDKTVERKC | CVECPPCPAP        | 250  |
| PVAGPSVFLF | PPKPKDTLMI | SRTPEVTCVV | VDVSHEDPEV | QFNWYVDGVE        | 300  |
| VHNAKTKPRE | EQFNSTFRVV | SVLTVVHQDW | LNGKEYKCKV | SNKGLPAPIE        | 350  |
| KTISKTKGQP | REPQVYTLPP | SREEMTKNQV | SLTCLVKGFY | <b>PSDIAVEWES</b> | 400  |
| NGQPENNYKT | TPPMLDSDGS | FFLYSKLTVD | KSRWQQGNVF | SCSVMHEALH        | 450  |
| NHYTQKSLSL | SPGK       |            |            |                   | 464  |

(SEQ ID NO:2)

# Figure 1B (continued)

# 4.8.1 Kappa Chain DNA

| <u>ATGGAAACCC</u> | <u>CAGCGCAG</u> CT | TCTCTTCCTC | CTGCTACTCT | GGCTCCCAGA | 50 · |
|-------------------|--------------------|------------|------------|------------|------|
| TACCACCGGA        | GAAATTGTGT         | TGACGCAGTC | TCCAGGCACC | CTGTCTTTGT | 100  |
| CTCCAGGGGA        | AAGAGCCACC         | CTCTCCTGCA | GGACCAGTGT | TAGCAGCAGT | 150  |
| TACTTAGCCT        | GGTACCAGCA         | GAAACCTGGC | CAGGCTCCCA | GGCTCCTCAT | 200  |
| CTATGGTGCA        | TCCAGCAGGG         | CCACTGGCAT | CCCAGACAGG | TTCAGTGGCA | 250  |
| GTGGGTCTGG        | GACAGACTTC         | ACTCTCACCA | TCAGCAGACT | GGAGCCTGAA | 300  |
| GATTTTGCAG        | TCTATTACTG         | TCAGCAGTAT | GGCATCTCAC | CCTTCACTTT | 350  |
| CGGCGGAGGG        | ACCAAGGTGG         | AGATCAAGCG | AACTGTGGCT | GCACCATCTG | 400  |
| TCTTCATCTT        | CCCGCCATCT         | GATGAGCAGT | TGAAATCTGG | AACTGCCTCT | 450  |
| GTTGTGTGCC        | TGCTGAATAA         | CTTCTATCCC | AGAGAGGCCA | AAGTACAGTG | 500  |
| GAAGGTGGAT        | AACGCCCTCC         | AATCGGGTAA | CTCCCAGGAG | AGTGTCACAG | 550  |
| AGCAGGACAG        | CAAGGACAGC         | ACCTACAGCC | TCAGCAGCAC | CCTGACGCTG | 600  |
| AGCAAAGCAG        | ACTACGAGAA         | ACACAAAGTC | TACGCCTGCG | AAGTCACCCA | 650  |
| TCAGGGCCTG        | AGCTCGCCCG         | TCACAAAGAG | CTTCAACAGG | GGAGAGTGTT | 700  |
| AG                | •                  |            |            |            | 702  |
|                   |                    |            |            |            |      |

(SEQ ID NO:41)

# 4.8.1 Kappa Chain Protein

| METPAQLLFL | LLLWLPDTTG | EIVLTQSPGT | LSLSPGERAT | LSCRTSVSSS | 50  |
|------------|------------|------------|------------|------------|-----|
| YLAWYQQKPG | QAPRLLIYGA | SSRATGIPDR | FSGSGSGTDF | TLTISRLEPE | 100 |
| DFAVYYCQQY | GISPFTFGGG | TKVEIKRTVA | APSVFIFPPS | DEQLKSGTAS | 150 |
| VVCLLNNFYP | REAKVQWKVD | NALQSGNSQE | SVTEQDSKDS | TYSLSSTLTL | 200 |
| SKADYEKHKV | YACEVTHOGL | SSPVTKSFNR | GEC        |            | 233 |

(SEQ ID NO:15)

# Figure 1C

# 4.14.3 Heavy Chain DNA

| ACCTTCAG 50   | GCGTCTGGAT   | CTCCTGTGCA  | CCCTGAGACT  | CCTGGGAGGT   |
|---|--|---|---|--|
| GCTGGAGT 100  | TCCAGGCAAG   | TCCGCCAGGC  | ATCCACTGGG  | TAGTCATGGC   |
| CAGACTCC 150  |  |   |   |  |
| ACGCTGTA 200  | AATTCCAAGA   | CTCCAGAGAC  | GATTCACCAT  | GTGAAGGGCC   |
| TTACTGTG 250  | CACGGCTGTG   | GAGCCGAGGA  | AACAGCCTGA  | TTTGCAAATG   |
| GAACCCTG 300  |  |   |   |  |
| CCCCTGGC 350  | CCATCGGTCT   | CACCAAGGGC  | CCTCAGCCTC  | GTCACCGTCT   |
| CTGCCTGG 400  | AGCGGCCCTG   | CCGAGAGCAC  | AGGAGCACCT  | GCCCTGCTCC   |
| CAGGCGCT 450  | TGTCGTGGAA   | CCGGTGACGG  | CTTCCCCGAA  | TCAAGGACTA   |
| 489   | GTCCTACAG  | CTTCCCAGCT  | GCGTGCACAC  | CTGACCAGCG   |
| ACGCTGTA 2 TTACTGTG 2 GAACCCTG 3 CCCCTGGC 3 CTGCCTGG 4 CAGGCGCT 4 | AATTCCAAGA<br>CACGGCTGTG<br>ACTGGGGCCA<br>CCATCGGTCT<br>AGCGGCCCTG<br>TGTCGTGGAA | CTCCAGAGAC GAGCCGAGGA CCACTTGACT CACCAAGGGC CCGAGAGCAC CCGGTGACGG | GATTCACCAT AACAGCCTGA CCCACTGGGG CCTCAGCCTC AGGAGCACCT CTTCCCCGAA | GTGAAGGCC TTTGCAAATG CGAGAGTGGC GTCACCGTCT GCCCTGCTCC TCAAGGACTA |

(SEQ ID NO:29)

# 4.14.3 Heavy Chain Protein

| PGRSLRLSCA | ASGFTFSSHG | IHWVRQAPGK | GLEWVAVIWY | DGRNKDYADS | 50  |
|------------|------------|------------|------------|------------|-----|
| VKGRFTISRD |            |            |            |            |     |
| VTVSSASTKG | PSVFPLAPCS | RSTSESTAAL | GCLVKDYFPE | PVTVSWNSGA | 150 |
| LTSGVHTFPA | VLQ        |            |            |            | 163 |

(SEQ ID NO:3)

#### 4.14.3 Kappa Chain DNA

| GGCACCCTGT | CTTTGTCTCC | AGGGGAAAGA | GCCACCCTCT | CCTGCAGGGC | 50  |
|------------|------------|------------|------------|------------|-----|
|            |            |            |            | AAACCTGGCC |     |
|            |            |            |            | CACTGGCATC |     |
| CCAGACAGGT | TCAGTGGCAG | TGGGTCTGGG | ACAGACTTCA | CTCTCACCAT | 200 |
|            |            |            |            | CAGCAGTATG |     |
|            |            |            |            | TATCAAGCGA |     |
|            |            |            |            | ATGAGCAGTT |     |
| GAAATCTGGA | ACTGCCTCTG | TTGTGTGCCT | GCTGAATAAC | TTCTATCCCA | 400 |
| GAGAGGCCAA | AGTACAG    | ,          |            |            | 417 |
|            |            |            |            |            |     |

(SEQ ID NO:42)

## 4.14.3 Kappa Chain Protein

| GTLSLSPGER | ATLSCRASQS | VSSYLAWYQQ | KPGQAPRLLI | YGASSRATGI | 50  |
|------------|------------|------------|------------|------------|-----|
| PDRFSGSGSG | TDFTLTISRL | EPEDFAVYYC | QQYGRSPFTF | GPGTKVDIKR | 100 |
| TVAAPSVFIF | PPSDEQLKSG | TASVVCLLNN | FYPREAKVQ  |            | 139 |

(SEQ ID NO:16)

# Figure 1D

#### 6.1.1 Heavy Chain DNA

```
ATGGAGTTTG GGCTGAGCTG GGTTTTCCTC GTTGCTCTTT TAAGAGGTGT 50
CCAGTGTCAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCGAGCCTG 100
GGAGGTCCCT GAGACTCTCC TGTACAGCGT CTGGATTCAC CTTCAGTAGT 150
TATGGCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT 200
GGCAGTTATA TGGTATGATG GAAGCAATAA ACACTATGCA GACTCCGCGA 250
AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC GCTGTATCTG 300
CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ACTGTGCGAG 350
AGCCGGACTG CTGGGTTACT TTGACTACTG GGGCCAGGGA ACCCTGGTCA 400
CCGTCTCCTC AGCCTCCACC AAGGGCCCAT CGGTCTTCCC CCTGGCGCCC 450
TGCTCCAGGA GCACCTCCGA GAGCACAGCG GCCCTGGGCT GCCTGGTCAA 500
GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCTCTGA 550
CCAGCGGCGT GCACACCTTC CCAGCTGTCC TACAGTCCTC AGGACTCTAC 600
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAACTTCG GCACCCAGAC 650
CTACACCTGC AACGTAGATC ACAAGCCCAG CAACACCAAG GTGGACAAGA 700
CAGTTGAGCG CAAATGTTGT GTCGAGTGCC CACCGTGCCC AGCACCACCT 750
GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CCAAAACCCA AGGACACCCT 800
CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC 850
ACGAAGACCC CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG 900
CATAATGCCA AGACAAAGCC ACGGGAGGAG CAGTTCAACA GCACGTTCCG 950
TGTGGTCAGC GTCCTCACCG TTGTGCACCA GGACTGGCTG AACGGCAAGG 1000
AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCCAGCCCC CATCGAGAAA 1050
ACCATCTCCA AAACCAAAGG GCAGCCCCGA GAACCACAGG TGTACACCCT 1100
GCCCCCATCC CGGGAGGAGA TGACCAAGAA CCAGGTCAGC CTGACCTGCC 1150
TGGTCAAAGG CTTCTACCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT 1200
GGGCAGCCGG AGAACAACTA CAAGACCACA CCTCCCATGC TGGACTCCGA 1250
CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC 1300
AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC 1350
CACTACACGC AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GA
```

(SEQ ID NO:30)

#### 6.1.1 Heavy Chain Protein

```
MEFGLSWVFLVALLRGVQCQVQLVESGGGVVEPGRSLRLSCTASGFTFSS50YGMHWVRQAPGKGLEWVAVIWYDGSNKHYADSAKGRFTISRDNSKNTLYL100QMNSLRAEDTAVYYCARAGLLGYFDYWGQGTLVTVSSASTKGPSVFPLAP150CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY200SLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPP250VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV300HNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEK350TISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN400GQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN450HYTQKSLSLSPGK463
```

# Figure 1D (continued)

#### 6.1.1 Kappa Chain DNA

```
ATGGAAACCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGA50TACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGT100CTCCAGGGGAAAGAGCCACCCTCTCCTGTAGGGCCAGTCAAAGTGTTAGC150AGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCCCCT200CATCTATGGTGTATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTG250GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCT300GAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTATCTCACCATTCAC350TTTCGGCCCTGGGACCAAAGTGGATATCAAACGAACTGTGGCTGCACCAT400CTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCC450TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA500GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCA550CAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACG650CTGAGCAGGCTGAGCTCGCCCGTCACAAAGTCTACGCCTGCGAAGTCAC650CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGT700GTTAGTTAGTTTAGTTTAGCTCAACAGGGGAGAGT700
```

(SEQ ID NO:43)

#### 6.1.1 Kappa Chain Protein

|            | LLLWLPDTTG |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| SYLAWYQQKP | GQAPRPLIYG | VSSRATGIPD | RFSGSGSGTD | FTLTISRLEP | 100 |
| EDFAVYYCQQ | YGISPFTFGP | GTKVDIKRTV | AAPSVFIFPP | SDEQLKSGTA | 150 |
| SVVCLLNNFY | PREAKVQWKV | DNALQSGNSQ | ESVTEQDSKD | STYSLSSTLT | 200 |
| LSKADYEKHK | VYACEVTHQG | LSSPVTKSFN | RGEC       |            | 234 |

(SEQ ID NO:17)

# Figure 1E

## 3.1.1 Heavy Chain DNA

| GGCGTGGTCC | AGCCTGGGAG | GTCCCTGAGA | CTCTCCTGTG | CAGCGTCTGG | 50  |
|------------|------------|------------|------------|------------|-----|
| ATTCACCTTC | AGTAGCTATG | GCATGCACTG | GGTCCGCCAG | GCTCCAGGCA | 100 |
| AGGGGCTGGA | GTGGGTGGCA | GTTATATGGT | ATGATGGAAG | TAATAAATAC | 150 |
| TATGCAGACT | CCGTGAAGGG | CCGATTCACC | ATCTCCAGAG | ACAATTCCAA | 200 |
| GAACACGCTG | TATCTGCAAA | TGAACAGCCT | GAGAGCCGAG | GACACGGCTG | 250 |
| TGTATTACTG | TGCGAGAGGG | GCCCGTATAA | TAACCCCTTG | TATGGACGTC | 300 |
| TGGGGCCAAG | GGACCACGGT | CACCGTCTCC | TCAGCCTCCA | CCAAGGGCCC | 350 |
| ATCGGTCTTC | CCCCTGGCGC | CCTGCTCCAG | GAGCACCTCC | GAGAGCACAG | 400 |
| CGGCCCTGGG | CTGCCTGGTC | AAGGACTACT | TCCCCGAACC | GGTGACGGTG | 450 |
| TCGTGGAACT | CAGGCGCTCT | GACCAGCGGC | GTGCACACCT | TCCCAGCTGT | 500 |
| CCTACAG    |            |            |            |            | 507 |
|            |            |            |            |            |     |

(SEQ ID NO:31)

## 3.1.1 Heavy Chain Protein

| GVVQPGRSLR | LSCAASGFTF | SSYGMHWVRQ | APGKGLEWVA | VIWYDGSNKY | 50  |
|------------|------------|------------|------------|------------|-----|
| YADSVKGRFT | ISRDNSKNTL | YLQMNSLRAE | DTAVYYCARG | ARIITPCMDV | 100 |
| WGQGTTVTVS | SASTKGPSVF | PLAPCSRSTS | ESTAALGCLV | KDYFPEPVTV | 150 |
| SWNSGALTSG | VHTFPAVLQ  |            |            |            | 169 |

(SEQ ID NO:5)

## 3.1.1 Kappa Chain DNA

| CAGTCTCCAT | CCTCCCTGTC | TGCATCTGTA | GGAGACAGAG | TCACCATCAC | 50. |
|------------|------------|------------|------------|------------|-----|
| TTGCCGGGCA | AGTCAGAGCA | TTAACACCTA | TTTAATTTGG | TATCAGCAGA | 100 |
| AACCAGGGAA | AGCCCCTAAC | TTCCTGATCT | CTGCTACATC | CATTTTGCAA | 150 |
| AGTGGGGTCC | CATCAAGGTT | CCGTGGCAGT | GGCTCTGGGA | CAAATTTCAC | 200 |
| TCTCACCATC | AACAGTCTTC | ATCCTGAAGA | TTTTGCAACT | TACTACTGTC | 250 |
|            |            |            |            | CAAAGTGGAT |     |
|            |            |            |            | CGCCATCTGA |     |
|            |            |            |            | CTGAATAACT |     |
|            |            |            |            | CGCCCTCCAA |     |
| TCGGGTAA   |            | •          |            |            | 458 |
|            |            |            |            |            |     |

(SEQ ID NO:44)

# 3.1.1 Kappa Chain Protein

| QSPSSLSASV | GDRVTITCRA | SQSINTYLIW | YQQKPGKAPN | FLISATSILQ | 50  |
|------------|------------|------------|------------|------------|-----|
| SGVPSRFRGS | GSGTNFTLTI | NSLHPEDFAT | YYCQQSYSTP | FTFGPGTKVD | 100 |
| IKRTVAAPSV | FIFPPSDEQL | KSGTASVVCL | LNNFYPREAK | VQWKVDNALQ | 150 |
| SG         |            |            |            |            | 152 |

# Figure 1F

## 4.10.2 Heavy Chain DNA

| GGCGTGGTCC | AGCCTGGGAG | GTCCCTGAGA | CTCTCCTGTG | TAGCGTCTGG | 50  |
|------------|------------|------------|------------|------------|-----|
| ATTCATCTTC | AGTAGTCATG | GCATCCACTG | GGTCCGCCAG | GCTCCAGGCA | 100 |
| AGGGGCTGGA | GTGGGTGGCA | GTTATATGGT | ATGATGGAAG | AAATAAAGAC | 150 |
| TATGCAGACT | CCGTGAAGGG | CCGATTCACC | ATCTCCAGAG | ACAATTCCAA | 200 |
| GAACACGCTG | TATTTGCAAA | TGAACAGCCT | GAGAGCCGAG | GACACGGCTG | 250 |
| TGTATTACTG | TGCGAGAGTG | GCCCCACTGG | GGCCACTTGA | CTACTGGGGC | 300 |
| CAGGGAACCC | TGGTCACCGT | CTCCTCAGCC | TCCACCAAGG | GCCCATCGGT | 350 |
| CTTCCCCCTG | GCGCCCTGCT | CCAGGAGCAC | CTCCGAGAGC | ACAGCGGCCC | 400 |
| TGGGCTGCCT | GGTCAAGGAC | TACTTCCCCG | AACCGGTGAC | GGTGTCGTGG | 450 |
| AACTCAGGCG | CTCTGACCAG | CGGCGTGCAC | ACCTTCCCAG | CTGTCCTACA | 500 |
| G          |            |            |            |            | 501 |

(SEQ ID NO:32)

## 4.10.2 Heavy Chain Protein

| GVVQPGRSLR | LSCVASGFIF | SSHGIHWVRQ | APGKGLEWVA | VIWYDGRNKD | 50  |
|------------|------------|------------|------------|------------|-----|
| YADSVKGRFT | ISRDNSKNTL | YLQMNSLRAE | DTAVYYCARV | APLGPLDYWG | 100 |
| QGTLVTVSSA | STKGPSVFPL | APCSRSTSES | TAALGCLVKD | YFPEPVTVSW | 150 |
| NSGALTSGVH | TFPAVLQ    |            |            |            | 167 |

(SEQ ID NO:6)

## 4.10.2 Kappa Chain DNA

| TCTCCAGGCA | CCCTGTCTTT | GTCTCCAGGG | GAAAGAGCCA | CCCTCTCCTG | 50  |
|------------|------------|------------|------------|------------|-----|
| CAGGGCCAGT | CAGAGTATTA | GCAGCAATTT | CTTAGCCTGG | TACCAGCAGA | 100 |
| AACCTGGCCA | GGCTCCCAGG | CTCCTCATCT | ATCGTCCATC | CAGCAGGGCC | 150 |
| ACTGGCATCC | CAGACAGTTT | CAGTGGCAGT | GGGTCTGGGA | CAGACTTCAC | 200 |
| TCTCACCATC | AGCAGACTGG | AGCCTGAGGA | TTTTGCATTA | TATTACTGTC | 250 |
| AGCAGTATGG | TACGTCACCA | TTCACTTTCG | GCCCTGGGAC | CAAAGTGGAT | 300 |
| ATCAAGCGAA | CTGTGGCTGC | ACCATCTGTC | TTCATCTTCC | CGCCATCTGA | 350 |
|            |            |            | TGTGTGCCTG | CTGAATAACT | 400 |
| TCTATCCCAG | AGAGGCCAAA | GTACAG     |            |            | 426 |
|            |            |            |            |            |     |

(SEQ ID NO:45)

## 4.10.2 Kappa Chain Protein

| SPGTLSLSPG | ERATLSCRAS | QSISSNFLAW | YQQKPGQAPR | LLIYRPSSRA | 50  |
|------------|------------|------------|------------|------------|-----|
| TGIPDSFSGS | GSGTDFTLTI | SRLEPEDFAL | YYCQQYGTSP | FTFGPGTKVD | 100 |
| IKRTVAAPSV | FIFPPSDEQL | KSGTASVVCL | LNNFYPREAK | VQ         | 142 |

(SEQ ID NO:19)

# Figure 1G

#### 2.1.3 Heavy Chain DNA

|            | GACTGGTGAA |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TGTCTCTGGT | GGCTCCATCA | GCAGTGGTGG | TCACTACTGG | AGCTGGATCC | 100 |
|            | AGGGAAGGGC |            |            |            |     |
|            | ACTACAACCC |            |            |            |     |
|            | AAGAACCAGT |            |            |            |     |
|            | CGTGTATTAT |            |            |            |     |
| ATAGACGTCT | GGGGCCAAGG | GACCACGGTC | ACCGTCTCCT | CAGCTTCCAC | 350 |
| CAAGGGCCCA | TCCGTCTTCC | CCCTGGCGCC | CTGCTCCAGG | AGCACCTCCG | 400 |
| AGAGCACAGC | CGCCCTGGGC | TGCCTGGTCA | AGGACTACTT | CCCCGAACCG | 450 |
| GTGACGGTGT | CGTGGAACTC | AGGCGCCCTG | ACCAGCGGCG | TGCACACCTT | 500 |
| CCCGGCTGTC | CTACAA     |            |            |            | 516 |
|            |            |            |            |            |     |

(SEQ ID NO:33)

## 2.1.3 Heavy Chain Protein

| SGPGLVKPSQ | ILSLTCTVSG | GSISSGGHYW | SWIRQHPGKG | LEWIGYIYYI | 50  |
|------------|------------|------------|------------|------------|-----|
| GNTYYNPSLK | SRVTISVDTS | KNQFSLKLSS | VTAADTAVYY | CARDSGDYYG | 100 |
| IDVWGQGTTV | TVSSASTKGP | SVFPLAPCSR | STSESTAALG | CLVKDYFPEP | 150 |
| VTVSWNSGAL | TSGVHTFPAV | LQ         |            |            | 172 |

(SEQ ID NO:7)

## 2.1.3 Kappa Chain DNA

| TCTCCAGACT | TTCAGTCTGT | GACTCCAAAG | GAGAAAGTCA | CCATCACCTG | 50  |
|------------|------------|------------|------------|------------|-----|
| CCGGGCCAGT | CAGAGCATTG | GTAGTAGCTT | ACATTGGTAT | CAGCAGAAAC | 100 |
| CAGATCAGTC | TCCAAAGCTC | CTCATCAAGT | ATGCTTCCCA | GTCCTTCTCT | 150 |
| GGGGTCCCCT | CGAGGTTCAG | TGGCAGTGGA | TCTGGGACAG | ATTTCACCCT | 200 |
| CACCATCAAT | AGCCTGGAAG | CTGAAGATGC | TGCAACGTAT | TACTGTCATC | 250 |
| AGAGTAGTAG | TTTACCGCTC | ACTTTCGGCG | GAGGGACCAA | GGTGGAGATC | 300 |
| AAACGAACTG | TGGCTGCACC | ATCTGTCTTC | ATCTTCCCGC | CATCTGATGA | 350 |
| GCAGTTGAAA | TCTGGAACTG | CCTCTGTTGT | GTGCCTGCTG | AATAACTTCT | 400 |
| ATCCCAGAGA | GGCCAAAGTA | CAGTGGAAGG | TGGATAACGC | CCTCCAATCG | 450 |
| GGTAACTCCC | AGGAG      |            |            |            | 465 |
|            |            |            |            |            |     |

(SEQ ID NO:46)

## 2.1.3 Kappa Chain Protein

| SPDFQSVTPK | EKVTITCRAS | QSIGSSLHWY | QQKPDQSPKL | LIKYASQSFS | 50  |
|------------|------------|------------|------------|------------|-----|
| GVPSRFSGSG | SGTDFTLTIN | SLEAEDAATY | YCHQSSSLPL | TFGGGTKVEI | 100 |
| KRTVAAPSVF | IFPPSDEQLK | SGTASVVCLL | NNFYPREAKV | QWKVDNALQS | 150 |
| GNSQE      |            |            |            |            | 155 |

(SEQ ID NO:20)

# Figure 1H

## 4.13.1 Heavy Chain DNA

|            |            |            |            | TCACCTTCAG. |     |
|------------|------------|------------|------------|-------------|-----|
|            |            |            |            | GGGCTGGAGT  |     |
|            |            |            |            | TGCAGACTCC  |     |
|            |            |            |            | ACACGCTGTA  |     |
|            |            |            |            | TATTACTGTG  |     |
|            |            |            |            | GGGAACCCTG  |     |
| GTCACCGTCT | CCTCAGCCTC | CACCAAGGGC | CCATCGGTCT | TCCCCCTGGC  | 350 |
|            |            |            |            | GGCTGCCTGG  |     |
| TCAAGGACTA | CTTCCCCGAA | CCGGTGACGG | TGTCGTGGAA | CTCAGGCGCT  | 450 |
| CTGACCAGC  |            |            |            |             | 459 |

(SEQ ID NO:34)

## 4.13.1 Heavy Chain Protein

| PGRSLRLSCA     | ASGFTFSSHG | IHWVRQAPGK | GLEWVAVIWY | DGRNKDYADS | 50  |
|----------------|------------|------------|------------|------------|-----|
| <br>VKGRFTISRD | NSKNTLYLQM | NSLRAEDTAV | YYCARVAPLG | PLDYWGQGTL | 100 |
| VTVSSASTKG     | PSVFPLAPCS | RSTSESTAAL | GCLVKDYFPE | PVTVSWNSGA | 150 |
| LTS            | ·          |            |            |            | 153 |

(SEQ ID NO:8)

## 4.13.1 Kappa Chain DNA

| CAGTCTCCAG | GCACCCTGTC | TTTGTCTCCA | GGGGAAAGAG | CCACCCTCTC | 50  |
|------------|------------|------------|------------|------------|-----|
| CTGCAGGGCC | AGTCAGAGTG | TCAGCAGCTA | CTTAGCCTGG | TACCAGCAGA | 100 |
| AACCTGGCCA | GGCTCCCAGG | CTCCTCATCT | ATGGTGCATC | CAGCAGGGCC | 150 |
|            |            | CAGTGGCAGT |            |            |     |
|            |            | AGCCTGAGGA |            |            |     |
|            |            | TTCACTTTCG |            |            |     |
|            |            | ACCATCTGTC |            |            | 350 |
| TGAGCAGTTG | AAATCTGGAA | CTGCCTCTGT | TGTGTGCCTG | CTGAATAACT | 400 |
| TCTATCCCAG | AGAGGCCAAA | GTACAGTGGA | AAGGTGGATA |            | 440 |

(SEQ ID NO:47)

#### 4.13.1 Kappa Chain Protein

| QSPGTLSLSP | GERATLSCRA | SQSVSSYLAW | YQQKPGQAPR | LLIYGASSRA | 50  |
|------------|------------|------------|------------|------------|-----|
| TGIPDRFSGS | GSGTDFTLTI | SRLEPEDFAV | YYCQQYGRSP | FTFGPGTKVD | 100 |
| IKRTVAAPSV | FIFPPSDEQL | KSGTASVVCL | LNNFYPREAK | VQWKGG     | 146 |

(SEQ ID NO:21)

# 11.2.1 Heavy Chain DNA

|                       |            |            |            | -     |
|-----------------------|------------|------------|------------|-------|
| GGCGTGGTCC AGCCTGGGAG | GTCCCTGAGA | CTCTCCTGTG | CAGCGTCTGG | 50    |
| ATTCACCTTC AGTAGCTATG | GCATGCACTG | GGTCCGCCAG | GCTCCAGGCA | 100   |
| AGGGGCTGGA GTGGGTGGCA | GTTATATGGT | ATGATGGAAG | TAATAAATAC | 150   |
| TATGCAGACT CCGTGAAGGG | CCGATTCACC | ATCTCCAGAG | ACAATTCCAA | 200   |
| GAACACGCTG TATCTGCAAA | TGAACAGCCT | GAGAGCCGAG | GACACGGCTG | 250   |
| TGTATTACTG TGCGAGAGAT | CCGAGGGGAG | CTACCCTTTA | CTACTACTAC | 300   |
| TACCGGTKGG ACGTCTGGGG | CCAAGGGACC | ACGGTCACCG | TCTCCTCAGC | 350   |
| CTCCACCAAG GGCCCATCGG | TCTTCCCCCT | GGCGCCCTGC | TCCAGGAGCA | 400   |
| CCTCCGAGAG CACAGCGGCC | CTGGGCTGCC | TGGTCAAGGA | CTACTTCCCC | 450   |
| GAACCGGTGA CGGTGTCGTG | GAACTCAGGC | GCTCTGACCA | GCGGCGTGCA | 500   |
| CAC                   |            | •          |            | . 503 |
|                       |            |            |            |       |
| (SEC ID NO.35)        |            | •          |            |       |

(SEQ ID NO:33)

# 11.2.1 Heavy Chain Protein

| GVVQPGRSLR | LSCAASGFTF | SSYGMHWVRQ | APGKGLEWVA | VIWYDGSNKY | 50  |
|------------|------------|------------|------------|------------|-----|
| YADSVKGRFT | ISRDNSKNTL | YLQMNSLRAE | DTAVYYCARD | PRGATLYYYY | 100 |
| YRXDVWGQGT | TVTVSSASTK | GPSVFPLAPC | SRSTSESTAA | LGCLVKDYFP | 150 |
| EPVTVSWNSG | ALTSGVH    |            |            |            | 167 |

(SEQ ID NO:9)

# 11.2.1 Kappa Chain DNA

|            | TGTCTGCATC |            |            |            | 50  |
|------------|------------|------------|------------|------------|-----|
|            | AGCATTAACA |            |            |            | 100 |
| GGAAAGCCCC | TAAACTCCTG | ATCTATGCTG | CATCCAGTTT | GCAAAGTGGG | 150 |
|            | GGTTCAGTGG |            |            |            | 200 |
| CATCAGCAGT | CTGCAACCTG | AAGATTTTGC | AACTTACTAC | TGTCAACAGT | 250 |
| ATTACAGTAC | TCCATTCACT | TTCGGCCCTG | GGACCAAAGT | GGAAATCAAA | 300 |
|            | CTGCACCATC |            |            |            | 350 |
| GTTGAAATCT | GGAACTGCCT | CTGTTGTGTG | CCTGCTGAAT | AACTTCTATC | 400 |
| CCAGAGAGGC | CAAAGTA    |            |            |            | 417 |

(SEQ ID NO:48)

# 11.2.1 Kappa Chain Protein

| PSSLSASVGD | RVTITCRASQ | SINSYLDWYQ | QKPGKAPKLL | IYAASSLQSG | 50  |
|------------|------------|------------|------------|------------|-----|
| VPSRFSGSGS | GTDFTLTISS | LQPEDFATYY | CQQYYSTPFT | FGPGTKVEIK | 100 |
| RTVAAPSVFI | FPPSDEQLKS | GTASVVCLLN | NFYPREAKV  |            | 139 |

(SEQ ID NO:22)

# Figure 1J

# 11.6.1 Heavy Chain DNA

| GGCGTGGTCC | AGCCTGGGAG | GTCCCTGAGA | CTCTCCTGTG | CAGCGTCTGG | 50  |
|------------|------------|------------|------------|------------|-----|
| ATTCACCTTC | AGTAGCTATG | GCATGCACTG | GGTCCGCCAG | GCTCCAGGCA | 100 |
| AGGGGCTGGA | GTGGGTGGCA | GTTATATGGT | ATGATGGAAG | TCATAAATAC | 150 |
| TATGCAGACT | CCGTGAAGGG | CCGATTCACC | ATCTCCAGAG | ACAATTCCAA | 200 |
| GAACACGCTG | TATCTGCAAA | TGAACAGCCT | GAGAGCCGAG | GACACGGCTG | 250 |
| TGTATTACTG | TGCGAGAGGC | GCTGTAGTAG | TACCAGCTGC | TATGGACGTC | 300 |
| TGGGGCCAAG | GGACCACGGT | CACCGTCTCC | TCAGCCTCCA | CCAAGGGCCC | 350 |
| ATCGGTCTTC | CCCCTGGCGC | CCTGCTCCAG | GAGCACCTCC | GAGAGCACAG | 400 |
| CGGCCCTGGG | CTGCCTGGTC | AAGGACTACT | TCCCCGAACC | GGTGACGGTG | 450 |
| T          |            |            |            |            | 451 |

(SEQ ID NO:36)

## 11.6.1 Heavy Chain Protein

| GVVQPGRSLR | LSCAASGFTF | SSYGMHWVRQ | APGKGLEWVA | VIWYDGSHKY | 50  |
|------------|------------|------------|------------|------------|-----|
| YADSVKGRFT | ISRDNSKNTL | YLQMNSLRAE | DTAVYYCARG | AVVVPAAMDV | 100 |
| WGQGTTVTVS | SASTKGPSVF | PLAPCSRSTS | ESTAALGCLV | KDYFPEPVTV | 150 |
| S          |            |            |            | •          | 151 |

(SEQ ID NO:10)

## 11.6.1 Kappa Chain DNA

| ACCCAGTCTC | CATCCTCCCT | GTCTGCATCT | GTAGGAGACA | GAGTCACCAT | 50  |
|------------|------------|------------|------------|------------|-----|
| CACTTGCCGG | GCAAGTCAGA | ACATTAGCAG | GTATTTAAAT | TGGTATCAAC | 100 |
| AGAAACCAGG | GAAAGCCCCT | AAGTTCCTGA | TCTATGTTGC | ATCTATTTTG | 150 |
| CAAAGTGGGG | TCCCATCAGG | GTTCAGTGCC | AGTGGATCTG | GGCCAGATTT | 200 |
| CACTCTNACC | ATCAGCAGTC | TGCAACCTGA | AGATTTTGCA | ACTTACTACT | 250 |
| GTCAACAGAG | TTACAGTACC | CCATTCACTT | TCGGCCCTGG | GACCAAAGTG | 300 |
| GATATCAAAC | GAACTGTGGC | TGCACCATCT | GTCTTCATCT | TCCCGCCATC | 350 |
| TGATGAGCAG | TTGAAATCTG | GAACTGCCTC | TGTTGTGTGC | CTGCTGAATA | 400 |
| AC         |            |            |            | •          | 402 |
|            |            |            |            |            |     |

(SEQ ID NO:49)

## 11.6.1 Kappa Chain Protein

| TQSPSSLSAS | VGDRVTITCR | ASQNISRYLN | WYQQKPGKAP | KFŁIYVASIL | 50  |
|------------|------------|------------|------------|------------|-----|
| QSGVPSGFSA | SGSGPDFTLT | ISSLQPEDFA | TYYCQQSYST | PFTFGPGTKV | 100 |
| DIKRTVAAPS | VFIFPPSDEQ | LKSGTASVVC | LLNN       |            | 134 |

(SEQ ID NO:23)

# Figure 1K

## 11.7.1 Heavy Chain DNA

| GTGGTCCAGC | CTGGGAGGTC | CCTGAGACTC | TCCTGTGCAG | CGTCTGGATT | 50  |
|------------|------------|------------|------------|------------|-----|
|            |            | TGCACTGGGT |            |            |     |
| GGCTGGAGTG | GGTGGCAGTT | ATATGGTCTG | ATGGAAGTCA | TAAATACTAT | 150 |
|            |            | ATTCACCATC |            |            |     |
|            |            | ACAGCCTGAG |            |            |     |
|            |            | ATGATAGTAG |            |            |     |
| GGCCAGGGAA | CCCTGGTCAC | CGTCTCCTCA | GCCTCCACCA | AGGGCCCATC | 350 |
| GGTCTTCCCC | CTGGCGCCCT | GCTCCAGGAG | CACCTCCGAG | AGCACAGCGG | 400 |
| CCCTGGGCTG | CCTGGTCAAG | GACTACTTCC | CCGAACCG   |            | 438 |

(SEQ ID NO:37)

#### 11.7.1 Heavy Chain Protein

| VVQPGRSLRL | SCAASGFTFS | SXGMHWVRQA | PGKGLEWVAV | IWSDGSHKYY | 50  |
|------------|------------|------------|------------|------------|-----|
| ADSVKGRFTI | SRDNSKNTLY | LQMNSLRAED | TAVYYCARGT | MIVVGTLDYW | 100 |
| GQGTLVTVSS | ASTKGPSVFP | LAPCSRSTSE | STAALGCLVK | DYFPEP     | 146 |

(SEQ ID NO:11)

#### 11.7.1 Kappa Chain DNA

| *ACCCAGTCTC | ראייר כייר כייר | GTCTGCATCT | CTACCACACA | CACTCACCAT | EΛ  |
|-------------|-----------------|------------|------------|------------|-----|
|             |                 |            |            |            |     |
| CACTTGCCGG  | GCAAGTCAGA      | GCATTTGCAA | CTATTTAAAT | TGGTATCAGC | 100 |
| AGAAACCAGG  | AAAAGCCCCT      | AGGGTCCTGA | TCTATGCTGC | ATCCAGTTTG | 150 |
| CAAGGTGGGG  | TCCCGTCAAG      | GTTCAGTGGC | AGTGGATCTG | GGACAGATTG | 200 |
| CACTCTCACC  | ATCAGCAGTC      | TGCAACCTGA | AGATTTTGCA | ACTTACTACT | 250 |
| GTCAACAGAG  | TTACACTACC      | CCATTCACTT | TCGGCCCTGG | GACCAGAGTG | 300 |
| GATATCGAAC  | GAACTGTGGC      | TGCACCATCT | GTCTTCATCT | TCCCGCCATC | 350 |
| TGATGAGCAG  | TTGAAATCTG      | GAACTGCCTC | TGTTGTGTGC | CTGCTGAATA | 400 |
| ACTTCTATCC  | CAGAGAGGCC      | AAAGTACAGT | GGAAGGTGGA | TAACGCCTAT | 450 |
| T           |                 |            | •          |            | 451 |

(SEQ ID NO:50)

## 11.7.1 Kappa Chain Protein

```
TQSPSSLSAS VGDRVTITCR ASQSICNYLN WYQQKPGKAP RVLIYAASSL 50
QGGVPSRFSG SGSGIDCTLT ISSLQPEDFA TYYCQQSYIT PFTFGPGTRV 100
DIERTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA KVQWKVDNAY 150
```

(SEQ ID NO:24)

# Figure 1L

# 12.3.1.1 Heavy Chain DNA

| TCCTGTGCAG     | CGTCTGGATT   | CACCTTCAGT | TACTATGGCG   | TCTGGGGGAG | 50  |
|----------------|--------------|------------|--------------|------------|-----|
|                | GCCTGGGAGG   | •          |              |            | 100 |
|                | GTAGCTATGG   |            |              |            | 150 |
|                | TGGGTGGCAG   |            |              |            | 200 |
|                | CGTGAAGGGC   |            |              |            | 250 |
|                | ATCTGCAAAT   | ,          |              |            | 300 |
|                | GCGAGAGACT   |            |              |            | 350 |
|                | CTGGGGCCAA   |            |              |            | 400 |
|                | CATCGGTCTT   |            |              |            | 450 |
|                | GCGGCCCTGG   |            |              |            | 500 |
|                | GTCGTGGAAC   | •          | •            |            | 550 |
| TTCCCAGCTG     |              | ICAGGCGCIC | IGACCAGCGG   | CGIGCACACC | 562 |
| TICCCAGCIG     | 10           |            |              |            | 302 |
| (SEQ ID NO:    | . 201        |            |              |            |     |
| (SEQ ID NO:    | : 30)        |            | •            |            |     |
| 12 2 1 1 114   | eavy Chain 1 | Protein    |              |            |     |
| TT. 3. T. T.   | savy chain i | LOCCIA     |              |            |     |
| SCCCITIODCR    | ST.RT.SCAASG | FTFSSVCVHW | VPOADGKGI.E  | WVAVIWYDGS | 50  |
| · <del>-</del> |              |            | <b>-</b>     | ARDSYYDFWS |     |
|                |              |            |              | AALGCLVKDY |     |
| _              | SGALTSGVHT   |            | FC3K313E31   | AALGCLVADI |     |
| FPEPVIVSWN     | SGALISGVAI   | FPAV       |              |            | 174 |
| (SEQ ID NO:    | . 1 2 )      |            |              |            |     |
| (SEQ ID NO:    | . 12)        |            |              |            | •   |
| 12 3 1 1 18:   | appa Chain I | מאר        |              |            |     |
| 12.3.1.1       | ppu chuan .  | 21111      |              |            |     |
| CCACTCTCCC     | TGCCCGTCAC   | CCTTGGACAG | CCGGCCTCCA   | TCTCCTGCAG | 50  |
| GTCTAGTCAA     | AGCCTCGTAT   | ACAGTGATGG | AAACACCTAC   | TTGAATTGGT | 100 |
| TTCAGCAGAG     | GCCAGGCCAA   | TCTCCAAGGC | GCCTAATTTA   | TAAGGTTTCT | 150 |
| AACTGGGACT     | CTGGGGTCCC   | AGACAGATTC | AGCGGCAGTG   | GGTCAGGCAC | 200 |
|                | CTGAAAATCA   |            |              |            | 250 |
|                | GCAAGGTTCA   |            |              |            | 300 |
|                | TCAAACGAAC   |            |              |            | 350 |
|                | GAGCAGTTGA   |            |              |            | 400 |
| TGAATAACTT     |              | AMICIGGAMC | IGCCICIGII   | GIGIGCCIGC | 419 |
| IGAAIAACII     | CIAICCCAC    |            |              |            | 413 |
| (SEQ ID NO     | . 511        |            |              |            |     |
| (SEQ ID NO     |              |            |              |            |     |
| 12 2 1 1 2.    | appa Chain I | Protein    |              | •          |     |
| 14.3.1.1 K     | spha chain   | TOCETH     |              |            |     |
|                | DACTCCDCCC   |            | LATITECOPPES | CDDDT TYPE |     |
| =              |              |            |              | SPRRLIYKVS | 50  |
| NWDSGVPDRF     | SGSGSGTDFT   | LKISKVEAED | VGVYYCMQGS   | HWPPTFGQGT | 100 |

139

(SEQ ID NO:25)

KVEIKRTVAA PSVFIFPPSD EQLKSGTASV VCLLNNFYP

# Figure 1M

# 12.9.1.1 Heavy Chain DNA

| GTCCAGCCTG | GGAGGTCCCT | GAGACTCTCC | TGTGCAGCGT | CTGGATTCAC | 50   |
|------------|------------|------------|------------|------------|------|
| CTTCAGTAAC | TATGCCATGC | ACTGGGTCCG | CCAGGCTCCA | GGCAAGGGGC | 100  |
| TGGAGTGGGT | GGTAGTTATT | TGGCATGATG | GAAATAATAA | ATACTATGCA | .150 |
| GAGTCCGTGA | AGGGCCGATT | CACCATCTCC | AGAGACAATT | CCAAGAACAC | 200  |
| GCTGTATCTG | CAAATGAACA | GCCTGAGAGC | CGAGGACACG | GCTGTATATT | 250  |
| ACTGTGCGAG | AGATCAGGGC | ACTGGCTGGT | ACGGAGGCTT | TGACTTCTGG | 300  |
| GGCCAGGGAA | CCCTGGTCAC | CGTCTCCTCA | GCCTCCACCA | AGGGCCCATC | 350  |
| GGTCTTCCCC | CTGGCGCCCT | GCTCCAGGAG | CACCTCCGAG | AGCACAGCGG | 400  |
| CCCTGGGCTG | CCTGGTCAAG | GACTACTTCC | CCGAACCGGT | GACGGTGTCG | 450  |
| TGGAACTCAG | GCGCTCTGAC | CAGCGGCGTG | CACACCTTCC |            | 490  |
|            |            |            |            |            |      |

(SEQ ID NO:39)

## 12.9.1.1 Heavy Chain Protein

| VQPGRSLRLS | CAASGFTFSN | YAMHWVRQAP | GKGLEWVVVI | WHDGNNKYYA | 50  |
|------------|------------|------------|------------|------------|-----|
| ESVKGRFTIS | RDNSKNTLYL | QMNSLRAEDT | AVYYCARDQG | TGWYGGFDFW | 100 |
| GQGTLVTVSS | ASTKGPSVFP | LAPCSRSTSE | STAALGCLVK | DYFPEPVTVS | 150 |
| WNSGALTSGV | HTF        |            |            |            | 163 |

(SEQ ID NO:13)

#### 12.9.1.1 Kappa Chain DNA

| CCTGGAGAGC | CGGCTTCCAT | CTCTTGCAGG | TCTAGTCAGA | GCCTCCTGCA | 50  |
|------------|------------|------------|------------|------------|-----|
| TAGTAATGGA | TACAACTATT | TGGATTGGTA | CCTGCAGAAG | CCAGGACAGT | 100 |
| CTCCACAGCT | CCTGATCTAT | TTGGGTTCTA | ATCGGGCCTC | CGGGGTCCCT | 150 |
| GACAGGTTCA | GTGGCAGTGG | ATCAGGCACA | GATTTTACAC | TGAAACTCAG | 200 |
| CAGAGTGGAG | GCTGAGGATG | TTGGGGTTTA | TTACTGCATG | CAAGCTCTAC | 250 |
| AAACTCCTCT | CACTTTCGGC | GGAGGGACCA | AGGTGGAGAT | CAAACGAACT | 300 |
| GTGGCTGCAC | CATCTGTCTT | CATCTTCCCG | CCATCTGATG | AGCAGTTGAA | 350 |
| ATCTGGAACT | GCCTCTGTTG | TGTGCCTGCT | GAATAACTTC | TATCCCAGAR | 400 |
| AGGCCAAAGT | ACATTCCAT  |            |            |            | 419 |

(SEQ ID NO:52)

## 12.9.1.1 Kappa Chain Protein

| PGEPASISCR | SSQSLLHSNG | YNYLDWYLQK | PGQSPQLLIY | LGSNRASGVP | 50  |
|------------|------------|------------|------------|------------|-----|
| DRFSGSGSGT | DFTLKLSRVE | AEDVGVYYCM | QALQTPLTFG | GGTKVEIKRT | 100 |
| VAAPSVFIFP | PSDEOLKSGT | ASVVCLLNNF | YPR        |            | 133 |

(SEQ ID NO:26)

# Figure 2A

| CDR                | DP5           | 3.1.1                         | 4.1.1                                    | 4.8.1    | 4.10.                  | 4.13.                                  | 4.14.  | 6.1.1  | 11.2.                                   | 11.6.     | 11.7.       | 12.3.                                   | 12.9.                                 |
|--------------------|---------------|-------------------------------|--|----------|------------------------|--|--------|--|---|-----------|-------------|---|---------------------------------------|
| CDR                | 0             | 3.1.1                         | 7.1.1                                    | 7.6.1    | 2                      | 1                                      | 3      | 0.1.1  | 11.2.                                   | 11.0.     | 11.7.       | 1.1                                     | 1.1                                   |
|                    |               |                               |  |          |                        | -                                      |        | G  |   |           |             |   |                                       |
|                    | G             | G                             | G  | G        | G                      |  |        | G  | G                                       | G         |             | G                                       | -                                     |
|                    | v             | V                             | v  | V        | V                      |  |        | V  | V                                       | V         | V           | V                                       |                                       |
|                    | V             | V                             | V  | V        | V                      |  |        | V  | V                                       | V         | V           | V                                       | V                                     |
|                    | Q             | Q                             | Q  | Q        | Q                      | -                                      |        | E  | Q                                       | Q         | Q           | Q                                       | Q                                     |
|                    | P             | P                             | P  | P        | P                      | P                                      | P      | P  | P                                       | P         | P           | P                                       | P                                     |
|                    | G             | G                             | G  | G        | G                      | G                                      | G      | G  | G                                       | G         | G           | G                                       | G                                     |
|                    | R             | R                             | R  | R        | R                      | R                                      | R      | R  | R                                       | R         | R           | R                                       | R                                     |
|                    | S             | S                             | S  | S        | S                      | S                                      | S      | S  | S                                       | S         | S           | S                                       | S                                     |
|                    | L             | L                             | L  | L        | L                      | L                                      | L      | L  | L                                       | L         | L           | L                                       | L                                     |
|                    | R             | R                             | R  | R        | R                      | R                                      | R      | R  | R                                       | R         | R           | R                                       | R                                     |
|                    | L             | L                             | L  | L        | L                      | L                                      | L      | L  | L                                       | L         | L           | L                                       | L_                                    |
|                    | S             | S                             | S  | S        | S                      | S                                      | S      | S  | S                                       | S         | S           | S                                       | S                                     |
|                    | С             | С                             | С  | С        | С                      | С                                      | С      | С  | C                                       | С         | С           | С                                       | С                                     |
|                    | A             | A                             | V  | T        | V                      | A                                      | A      | T  | A                                       | A         | A           | A                                       | _A_                                   |
|                    | A             | A                             | A  | A        | A                      | A                                      | A      | A  | A                                       | A         | A           | Α.                                      | A                                     |
|                    | S             | S                             | S  | S        | S                      | S                                      | S      | S  | S                                       | S         | S           | S                                       | S                                     |
| 2                  |               | G                             | G  | G<br>F   | G<br>F                 | G<br>F                                 | G<br>F | G<br>F   | G                                       | G<br>F    | G<br>F      | G<br>F                                  | G<br>F                                |
|                    | E<br>T        | F<br>T                        | F<br>T                                   | T        | I                      | T                                      | F<br>T | T  | F                                       | r         | T           | 26 that of with me the                  | T                                     |
|                    | F             | F                             | F  | F        | F                      | F                                      | F      | F.   | Ē                                       | F         | F           | T<br>F                                  | F                                     |
| CDR1               | ·S            | S                             | S  | S        | S                      | S                                      | S      | S  | S                                       | S         | S           | S                                       | S                                     |
| CDKI               | S %           | S                             | 'S                                       | N        | S                      | S                                      | S      | Ŝ  | S                                       | S         | S           | S                                       | N                                     |
| # 1 m              | Y             | · V                           | H  | Y        | H                      | н                                      | H      | Y  | Y                                       | Y         | C           | Y                                       | Y                                     |
|                    | . G.          | G                             | G  | G.       | G                      | G                                      | ·G     | G  | G                                       | G         | G           | G                                       | A                                     |
|                    | M             | М                             | М  | М        | 1                      | 71.2                                   | 11     | М  | М                                       | М         | M           | V                                       | M                                     |
|                    | H             | H                             | H  | Н        | н                      | Н                                      | H      | Н  | Н                                       | Н         | Н           | H                                       | Н                                     |
|                    | W             | W                             | W  | W        | W                      | W                                      | w      | W  | W                                       | W         | W           | W                                       | w                                     |
|                    | V             | V                             | V  | V        | V                      | V                                      | V      | V  | V                                       | V         | V           | V                                       | V                                     |
|                    | R             | R                             | R  | R        | R                      | R                                      | R      | R  | R                                       | R         | R           | R                                       | ·R                                    |
|                    | Q             | Q                             | Q  | Q        | Q                      | Q                                      | Q      | Q  | Q                                       | Q         | Q           | Q                                       | Q                                     |
|                    | Α             | Α                             | Α  | Α        | Α                      | Α                                      | Α      | Α  | Α                                       | Α         | Α           | Α                                       | Α                                     |
|                    | P             | P                             | P  | P        | P                      | P                                      | P      | P  | P                                       | P         | P           | P                                       | _ P                                   |
|                    | G             | G                             | G  | G        | G                      | G                                      | G      | G  | G                                       | G         | G           | G                                       | G                                     |
|                    | K             | K                             | K  | K        | K                      | K                                      | K      | K  | K                                       | K         | K           | K                                       | K                                     |
|                    | G             | G                             | G  | G        | G                      | G                                      | G      | G  | G                                       | G         | G           | G                                       | G                                     |
|                    | L             | L                             | L  | L        | L                      | L                                      | L      | L  | L                                       | L         | L           | L                                       | L                                     |
|                    | E             | E                             | E  | E        | E                      | E                                      | E      | E  | E                                       | E         | E           | E                                       | E                                     |
|                    | W             | W                             | W  | W        | W                      | W                                      | W      | W  | W                                       | W         | W           | W                                       | W                                     |
|                    | V             | V                             | V  | V        | V                      | V                                      | V      | V  | V                                       | V         | V           | V                                       | V                                     |
|                    | A<br>5 V      | A<br>V                        | A<br>V                                   | A<br>V   | A<br>V                 | A<br>V                                 | A<br>V | A  | A<br>V                                  | A<br>V    | A           | A<br>V                                  | V                                     |
| 7.297              | A I           | Ī                             | V<br>L                                   | Z I      | · V                    | I V                                    | · I    | · I  | ······································· | , v       | I T         | Ĭ                                       | V<br>I                                |
|                    | W             | W                             | W  | W        | W "                    | W                                      | Wes    | W  | W                                       | W         | W           | W                                       | W                                     |
|                    | Y             | Y                             | Ý  | Y        | Y                      | Y                                      | Y      | Y  | Y                                       | Y         | S           | Y                                       | H                                     |
| 33.3               | D             | D                             | D  |          | .D                     | D                                      | D      | · D  | √D.                                     | D.        | D           | ⊘ D                                     | D                                     |
|                    | © G,:-        | G                             |  | G        | √G                     | G                                      | G.∂    | G  | G.                                      | G         | G           | G                                       | G                                     |
| CDR2               |               | 10000000000000000000000000000 |  |          | R                      | R                                      |        |  | S)                                      | S         | S           | S //                                    |                                       |
| Mille and the same | 19000 75 3660 | 2                             | 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1 | TOTAL OF | Section of the Section | ************************************** | 12     | THE PARTY OF THE P | A STATE OF THE SECOND                   | 7.47 7.78 | Co and with | 100 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 1000000000000000000000000000000000000 |

# Figure 2B

| CDR      | DP5    | 3.1.1  | 4.1.1  | 4.8.1                                   | 4.10.    | 4.13.         | 4.14.                                   | 6.1.1                         | 11.2.                 | 11.6.                                   | 11.7.                                      | 12.3.                                   | 12.9.    |
|----------|--------|--|--|---|----------|---------------|---|-------------------------------|-----------------------|---|--|---|----------|
|          | 0      | NT.  | N.   | N :                                     | 2<br>N   | 1             | 3<br>N                                  | 2538100                       | 1<br>N                | 1<br>H                                  | 1  | 1.1<br>N                                | 1.1      |
|          | N<br>K | N  | K  | K                                       |          | · N · · · K   | K                                       | N<br>K                        | K                     | K                                       | H<br>K                                     | K                                       | · N<br>K |
|          | Y      | Y  |  | 700000000000000000000000000000000000000 | 270      |               | The second second                       |                               | Y                     | V V                                     | Y  | Y                                       |          |
| 44       | Ϋ́     | Y  | Y  | H<br>Y                                  | <b>D</b> | D             | y<br>Y                                  | H<br>Y                        | and the second second | Y                                       | Y  | Y<br>≤.Y                                | Y        |
|          |        | Someway and America  | Selection of the select |   | Y        | <u> Y</u>     | 2000 2000 0020 00 -                     | Service of college Service To | Y                     | T. W. COST OF THE PARTY OF THE PARTY OF | 200 14 14 14 14 14 14 14 14 14 14 14 14 14 | *************************************** | Y<br>A   |
|          | A      | A  | * A  | G                                       | A        | A             | A                                       | A                             | D.                    | A D                                     | A  | A                                       |          |
|          | D      | ≪D   | D.   | D.                                      | D O      | D             | Ž D                                     | D ·                           | A 200 ANTONIA         |   | D  | D                                       | E        |
|          | e s    | S  | S  | S                                       | S        | S             | S                                       | S                             | S                     | ⟨S <sup>2</sup>                         | isS :                                      | S                                       | S        |
|          | V      | V (  | V  | V                                       | V.       | V             | V                                       | A                             | V                     | V A                                     | V.   | V: :                                    | V        |
|          | K      | <u>K</u>   | K  | K                                       | K        | K             | K                                       | K                             | K                     | K                                       | K  | K                                       | K        |
|          | G      | G  | G  | G                                       | G        | G             | G                                       | G                             | G                     | G                                       | G  | G                                       | G        |
| <u> </u> | R      | R  | R  | R                                       | R        | R             | R                                       | R                             | R                     | R                                       | R  | R                                       | R        |
|          | F      | F  | F  | F                                       | F        | F             | F                                       | F                             | F                     | F                                       | F  | F                                       | F        |
|          | T      | T  | T  | T                                       | T        | T             | T                                       | Ţ                             | T                     | T                                       | T  | T                                       | T        |
| <u> </u> | I      | I  | I  | I                                       | I        | I             | I                                       | I                             | I                     | I                                       | I  | I                                       | I        |
| <u> </u> | S      | S  | S  | S                                       | S        | S             | S                                       | S                             | S                     | S                                       | S  | S                                       | S        |
|          | R      | R  | R  | S                                       | R        | R             | R                                       | R                             | R                     | R                                       | R  | R                                       | R        |
|          | D      | D  | D  | D                                       | D        | D             | D                                       | D                             | D                     | D                                       | D  | D                                       | D        |
|          | N      | N  | N  | N                                       | N        | N             | N                                       | N                             | N                     | N                                       | N  | N                                       | N        |
|          | S      | S  | S  | S                                       | S        | S             | S                                       | S                             | S                     | S                                       | S  | S                                       | S        |
|          | K      | K  | K  | K                                       | K        | K             | K                                       | K                             | K                     | K                                       | K  | K                                       | K        |
| <u> </u> | N      | N  | N  | N                                       | N        | N             | K                                       | N                             | N                     | N                                       | N  | S                                       | N        |
|          | T      | <u>T</u>   | T  | T                                       | T        | T             | T.                                      | T                             | T                     | T                                       | T  | T                                       | T        |
|          | L      | L  | L  | L                                       | L        | L             | L                                       | L                             | L                     | L                                       | L  | L                                       | L        |
|          | Y      | Y  | F  | Y                                       | Y        | Y             | Y                                       | Y                             | Y                     | Y                                       | Y  | Y                                       | Y        |
|          | L      | L  | L  | L                                       | L        | L             | L                                       | L                             | L                     | L                                       | L  | L                                       | L        |
|          | Q      | Q  | Q  | Q                                       | Q        | Q             | Q_                                      | Q                             | Q                     | Q                                       | _Q_  | Q                                       | Q        |
|          | M      | M  | M  | M                                       | M        | M             | M                                       | M                             | M                     | M                                       | M  | M                                       | M        |
|          | N      | N  | N  | N                                       | N        | N             | N                                       | N                             | N                     | N                                       | N  | N                                       | N        |
|          | S      | S  | S  | S                                       | S        | S             | S                                       | S                             | S                     | S                                       | S  | S                                       | S        |
|          | L      | L  | L  | L                                       | L        | L             | L                                       | L                             | L                     | L                                       | L  | L                                       | L        |
|          | R      | R  | R  | R                                       | R        | R             | R                                       | R                             | R                     | R                                       | R  | R                                       | R        |
|          | Α      | Α  | A  | - A                                     | Α        | A             | A                                       | Α                             | Α                     | Α                                       | Α  | Α                                       | A        |
|          | Е      | Е  | E  | E                                       | E        | E             | E                                       | E                             | E                     | E                                       | E  | E                                       | E        |
|          | D      | D  | D  | D                                       | D        | D             | D                                       | D                             | D                     | D                                       | D  | D                                       | D        |
|          | T      | T  | Т  | T                                       | T        | Т             | T                                       | T                             | T                     | T                                       | T  | T                                       | T        |
|          | Α      | Α  | Α  | Α                                       | Α        | Α             | A                                       | Α                             | Α                     | Α                                       | Α  | Α                                       | Α        |
|          | V      | V  | V  | V                                       | V        | V             | V                                       | V                             | V                     | V                                       | V  | V                                       | V        |
|          | Y      | Y  | Y  | Y                                       | Y        | Y             | Y                                       | Y                             | Y                     | Y                                       | Y  | Y                                       | Y        |
|          | Y      | Y  | Y  | Y                                       | Y        | Y             | Y                                       | Y                             | Y                     | Y                                       | Y  | Y                                       | Y        |
|          | С      | С  | С  | С                                       | С        | C             | С                                       | C                             | С                     | С                                       | С  | С                                       | С        |
|          | Α      | Α  | Α  | Α                                       | Α        | Α             | A                                       | Α                             | A                     | Α                                       | Α  | Α                                       | Α        |
|          | R      | R  | · R  | R                                       | R        | R             | R                                       | R                             | R                     | R                                       | R  | R                                       | R        |
| 100      | 44     | G F  | ∘G ∴   | $G \sim$                                | . V      | ∜ <b>V</b> ′  | V                                       | A                             | · Dy                  | G.                                      |  | D                                       | D.,      |
|          |        | A  | G  | · E                                     | A        | A             | A                                       | G                             | P                     | Α.                                      | OT:  | . S                                     |          |
|          |        | R  | ₹H   | R                                       | . P      | * <b>'P</b> ' | *************************************** | E.                            | R                     | V                                       | M  | Y                                       | ∕"∖G     |
|          |        | 3 1  | <b>F</b> ,   | L.                                      | L        | ·L,           | ξ.L.                                    | L                             | : G                   | V                                       | L  | ≤°Y                                     | T        |
| CDR3     | 100    | $\mathcal{I}_{I}}}}}}}}}}$ | G  | · · · · · ·                             | %.G ⊘    | G             | G                                       | $G_{i+1}$                     | : `A                  | · V                                     | V  | $D_{>g}$                                | G        |

Figure 2C

| CDR         | DP5  | 3.1.1 | 4.1.1            | 4.8.1 | 4.10.              | 4.13.          | 4.14. | 6.1.1  | 11.2.            | 11.6. | 11.7.  | 12.3.                | 12.9.        |
|-------------|--|-------|------------------|-------|--------------------|----------------|-------|--|------------------|-------|--------|----------------------|--------------|
|             | 0  |       |                  |       | 2                  | 1              | 3     |  | 1                | 1     | 1      | 1.1                  | 1.1          |
|             | 188  | T     | P                | S     | P                  | P              | P     | . Y  | T                | P     | V      | F                    | W            |
|             | 14(4)  | P     | $\mathbf{F}^{*}$ | Y     | L                  | L <sub>2</sub> | . L., | E. &   |                  | A     | ⊬, G 🗼 | W                    | Y            |
|             | g till   | C     | D                | F     | D. "               | $\mathbf{D}$   | D     | D  | Y                | A     | T      | S                    | G            |
|             | Vig 19.  | M     | Y                | · D.  | $\mathbf{Y}_{i,j}$ | Y              | . Y   | γY   | Y                | ·M    | L      | G                    | G.           |
|             |  | D     | W                | Y     | W                  | W              | W     | W  | Y                | D     | D      | R                    | % <b>F</b> ≤ |
|             |  | • V   | G                | W     | G                  | G              | G     | G  | Y                | · V   | Y      | G.                   | D            |
|             |  | W     | Q                | G     | Q                  | Q              | Q     | Q  | Y                | W     | W      | G.                   | F            |
|             |  | G     | G                | Q     | G                  | G              | G     | G  | G:               | G     | G      | M                    | W            |
|             |  | Q     | T                | G     | T                  | T              | T     | T  | M                | Q     | Q      | $\cdot$ $\mathbf{D}$ | G            |
|             |  | G     | L                | T     | L                  | L              | L     | L  | $\mathbf{D}_{m}$ | G     | G      | V                    | Q            |
|             |  | T     | V                | L     | V                  | V              | V     | V  | V                | T     | T      | W                    | G            |
|             |  | T     | T                | V     | Т                  | Τ.             | T     | T  | W                | T     | L      | G                    | T            |
|             |  | V     | V                | T     | V                  | V              | V     | V  | G                | V     | V      | Q                    | L            |
|             |  | T     | S                | V     | S                  | S              | S     | S  | Q                | T     | Т      | G                    | V            |
|             |  | V     | S                | S     | S                  | S              | S     | S  | G                | V     | V      | T                    | T            |
|             |  | S     | Α                | S     | Α                  | Α              | Α     | Α  | Т                | S     | S      | T                    | V            |
|             |  | S     | S                | A     | S                  | S              | S     | S  | T                | S     | S      | V                    | S            |
|             |  | Α     | T                | S     | T                  | T              | Т     | Т  | V                | A     | Α      | T                    | S            |
|             |  | S     | K                | T     | K                  | K              | K     | K  | T                | S     | S      | V                    | A            |
|             |  | T     | G                | K     | G                  | G              | G     | G  | V                | T     | Т      | S                    | S            |
|             | -  | K     | P                | G     | P                  | P              | P     | P  | S                | K     | K      | S                    | T            |
|             |  | G     | S                | P     | S                  | S              | S     | S  | S                | G     | G      | Α                    | K            |
|             |  | P     | V                | S     | V                  | V              | V     | V  | A                | P     | P      | S                    | G            |
|             |  | S     | F                | V     | F                  | F              | F     | F  | S                | S     | S      | T                    | P            |
|             |  | V     | P                | F     | P                  | P              | P     | P  | Т                | V     | V      | K                    | S            |
|             |  | F     | L                | P     | L                  | L              | L     | L  | K                | F     | F      | G                    | V            |
|             |  | P     | Α                | L     | A                  | A              | A     | Α  | G                | P     | P      | P                    | F            |
|             |  | L     | P                | A     | P                  | P              | P     | P  | P                | L     | L      | S                    | P            |
|             |  | Α     | С                | P     | C                  | C              | С     | C  | S                | A     | A      | V                    | L            |
|             |  | P     | S                | С     | S                  | S              | S     | S  | v                | P     | P      | F                    | A            |
|             |  | С     | R                | S     | R                  | R              | R     | R  | F                | С     | С      | P                    | P            |
|             |  | S     | S                | R     | S                  | S              | S     | S  | P                | S     | S      | L                    | С            |
|             |  | R     | T                | S     | T                  | T              | T     | T  | L                | R     | R      | A                    | S            |
|             |  | S     | S                | T     | S                  | S              | S     | S  | A                | S     | S      | P                    | R            |
|             |  | T     | E                | S     | E                  | E              | E     | E  | P                | T     | T      | C                    | S            |
|             |  | S     | S                | E     | S                  | S              | S     | S  | C                | s     | S      | S                    | T            |
|             |  | E     | T                | s     | T                  | T              | T     | T  | S                | E     | E      | R                    | S            |
|             |  | S     | A                | T     | A                  | Ā              | A     | A  | R                | S     | S      | S                    | E            |
| <del></del> |  | T     | A                | A     | A                  | A              | A     | A  | S                | T     | T      | T                    | S            |
|             |  | Ā.    | L                | A     | L                  | L              | L     | L  | T                | Ā     | A      | S                    | T            |
|             | <del> </del>                                     | A     | G                | L     | G                  | G              | G     | G  | S                | A     | A      | E                    | A            |
|             | <del> </del>                                     | L     | Č                | G     | C                  | C              | C     | C  | E                | L     | L      | S                    | A            |
|             | <u> </u>   | G     | L                | C     | L                  | L              | L     | L  | S                | G     | G      | T                    | L            |
|             |  | C     | v                | L     | V                  | V              | V     | <del> </del>                                     | T                | Ċ     | C      | A                    | G            |
|             |  | L     | K                | V     | K                  | K              | K     | 1  | A                | L     | L      | A                    | C            |
|             | <del>                                     </del> | v     | D                | K     | D                  | D              | D     | †  | A                | V     | V      | L                    | L            |
| <del></del> |  | K     | Y                | D     | Y                  | Y              | Y     | <del>                                     </del> | L                | K     | K      | G                    | V            |
| I           |  | . 41  |                  | 1     |                    | 1 1            |       | 1  | 1 -              | 1 1   |        | J 3                  |              |
|             |  | D     | F                | Y     | F                  | F              | F     |  | G                | D     | D      | С                    | K            |

Figure 2D

| CDR | DP5 | 3.1.1 | 4.1.1 | 4.8.1 | 4.10. | 4.13.    | 4.14. | 6.1.1    | 11.2. | 11.6.    | 11.7. | 12.3. | 12.9. |
|-----|-----|-------|-------|-------|-------|----------|-------|----------|-------|----------|-------|-------|-------|
|     | 0   |       |       |       | 2     | 1        | 3     |          | 1     | 1        | 1     | 1.1   | 1.1   |
|     |     | F     | Е     | P     | E     | E        | Е     |          | L     | F        | F     | V     | Y     |
|     |     | P     | P     | E     | P     | P        | P     |          | V     | P        | P     | K     | F     |
|     |     | E     | V     | P     | V     | V        | V     |          | K     | Е        | Е     | D     | P     |
|     |     | P     | T     | V     | T     | T        | T     |          | D     | P        | P     | Y     | E     |
|     |     | V     | V     | T     | V     | V        | V     |          | Y     | V        |       | F     | P     |
|     |     | T     | S     | V     | S     | S        | S     |          | F     | T        |       | P     | V     |
|     |     | V     | W     | S     | W     | W        | W     |          | P     | V        |       | Е     | T     |
|     |     | S     | N     | W     | N     | N        | N     |          | E     |          |       | P     | , V   |
|     |     | W     | S     | N     | S     | S        | S     |          | P     |          |       | V     | S     |
|     |     | · N   | G     | S     | G     | G        | G     |          | V     |          |       | T _   | W     |
|     |     | S     | A     | G     | Α     | Α        | Α     |          | T     |          |       | V     | N     |
|     |     | G     | L     | Α     | L     | L        | L     |          | V     |          |       | S     | S     |
|     |     | Α     | T     | L     | T     | T        | T     |          | S     |          |       | W     | G     |
|     |     | L     | S     | T     | S     | S        | S     |          | W     |          |       | N     | Α     |
|     |     | T     | G     | S     | G     |          | G     |          | N     |          |       | S     | L     |
|     |     | S     | V     | G     | V     |          | V     | <u> </u> | S     | ļ        |       | G     | T     |
|     |     | G     | H     | V     | H     |          | H     |          | G     |          |       | A     | S     |
|     |     | V     | T     | H     | T     |          | Т     |          | A     | <u> </u> |       | L     | G     |
|     |     | H     | F     | T     | F     |          | F     |          | L     |          |       | T     | V     |
|     |     | T     | P     | F     | P     | <u> </u> | P     |          | T     |          |       | S     | H     |
|     |     | F     | A     | P     | A     | <u> </u> | A     |          | S     |          |       | G     | T     |
|     |     | P     | V     | Α     | V     |          | V     |          | G     |          | ļ     | V     | F     |
|     |     | Α     | L     | V     | L     |          | L     |          | V     |          |       | H     |       |
|     |     | V     | Q     |       | Q     | İ        | Q     |          | H     |          |       | Т     |       |
|     |     | L     |       |       |       |          |       |          |       |          |       | F     |       |
|     |     | Q     |       |       |       |          |       |          | L     |          |       | P     |       |
|     |     |       |       |       |       |          |       |          |       |          |       | Α     |       |
|     |     |       |       |       |       |          |       |          |       |          |       | V     |       |
|     |     |       |       |       | L     |          |       | 1        |       |          |       |       |       |

DP-65 or 4-31 gene product

VSGGSI<u>SSGGYYW</u>SWIRQHPGKGLEWI<u>GYIYYSGSTYYNPSLKS</u>RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR CDR1

2.1.3 Heavy Chain Protein

SGPGLVKPSQILSLTCTVSGGS<u>ISSGGHYWS</u>WIRQHPGKGLEW<u>IGYIXYJGNTYYNPSLKS</u>RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR CDR1 DSGDYYGID<u>V</u>WGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ CDR3

|               | VYYCOOYGSSP   | CDR3 |
|---------------|---|------|
|               | YLAWYQQKPGQAPRLLIYGASSRATGPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOOYGSSP |      |
|               | PDRFSGSGSGTDI   |      |
|               | LLIYGASSRATGI   | CDR2 |
|               | WYQQKPGQAPR   |      |
|               | SOSVSSS   | CDR1 |
| fuct          | SLSPGERATLSCRA  |      |
| A27 Gene Proc | EIVLTQSPGTL   |      |

4.1.1 Kappa Chain Protein QSPGTLSLSPGERATLSCRASOSISSSELAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPWI FGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK <u>4.8.1 Kappa Chain Protein</u> QSPGTLSLSPGERATLSC<u>RTS00VSSSYLA</u>WYQQKPGQAPRLLIY<u>GASSRAT</u>GIPDRFSGSGSGTDFTLTISRLEPEDFAVYY<u>CQQYGISPF</u>T FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

GTLSLSPGERATLSC<u>RASOSVØSSYLA</u>WYQQKPGQAPRLLIY<u>GASSRAT</u>GIPDRFSGSGSGTDFTLTISRLEPEDFAVYY<u>CQQYGRSPFI</u> FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ 4.14.3 Kappa Chain Protein

6.1.1 Kappa Chain Protein QSPGTLSLSPGERATLSC<u>RASQSV0SSYLA</u>WYQQKPGQAPRPLIY<u>GVSSRA</u>TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYY<u>CQQYGISPFT</u> FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

4.10.2 Kappa Chain Protein SPGTLSLSPGERATLSCRASOSISSNFLAWYQQKPGQAPRLLIYRPSSRATGIPDSFSGSGSGTDFTLTISRLEPEDFALYYCQQYGTSPFT FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

QSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGRSPET FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKGG CDR1 4.13.1 Kappa Chain Protein

# 012 Gene Product

DIQMTQSPSSLSASVGDRVTITC<u>RASQSISSYL</u>NWYQQKPGKAPKLLIY<u>AASSLQS</u>GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC<u>QOSYST</u>

# 3.1.1 Kappa Chain Protein

QSPSSLSASVGDRVTITC<u>RASQSINTYLI</u>WYQQKPGKAPNFLIS<u>ATSILQS</u>GVPSRFRGSGSGTNFTLTINSLHPEDFATYYCQ<u>QSYSTPE</u> FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG CDR1

# 11.2.1 Kappa Chain Protein

PSSLSASVGDRVTITC<u>RASOSINSYLD</u>WYQQKPGKAPKLIYA<u>ASSLOS</u>GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC<u>QQYYSTPF</u> FGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV CDR1

# 11.6.1 Kappa Chain Protein

TQSPSSLSASVGDRVTITC<u>RASQNISRYL</u>NWYQQKPGKAPKFLIY<u>YASILQS</u>GVPS**G**FSASGSGPDFTLTISSLQPEDFATYYC<u>QQSYSTPF</u> FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN

# 11.7.1 Kappa Chain Protein

TQSPSSLSASVGDRVTITC<u>RASQSICNYL</u>NWYQQKPGKAPRVLIY<u>AASSLOG</u>GVPSRFSGSGSGIDCTLTISSLQPEDFATYYC<u>QOSYIIPE</u> FGPGTRVDIERTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAY CDR2

# A10/A26 Gene Product

EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLPQ CDR3

# 2.1.3 Kappa Chain Protein

SPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHOSSSLPLT CDR3 FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE

# A17 Gene Product

DVVMTQSPLSLPVTLGQPASISCRSSOSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP CDR3

12.3.1 Kappa Chain Protein
PLSI.PVTI.GQPASISCRSSQSI.VYSDGNTYI.NWFQQRPGQSPRRI.IYKVSNWDSGVPDRFSGSGSGTDFTI.KISRVEAEDVGVYYCMQGSHWPPT
CTNR?

CDR3

FGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP

# A3/A19 Gene Product

DIVMTQSPLSLPVTPGEPASISCRSSQSI\_LHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP CDR1

# 12.9.1 Kappa Chain Protein

PGEPASISCRSSOSI LHSNGYNYI DWYLQKPGQSPQLLIYI GSNRASGVPDRFSGSGSGTDFTLKLSRVEAEDVGVYYCMQALQTPLT CDR1 FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR

Figure 9 Amino-terminal amino acid sequence analysis

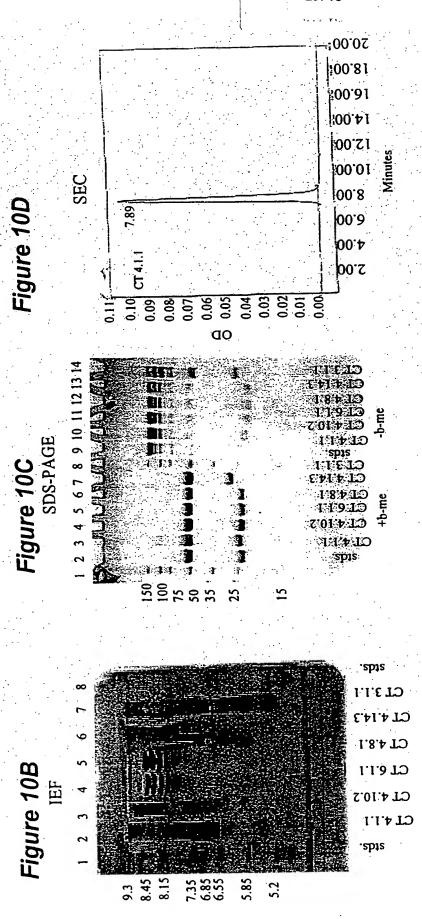
| Hybridoma | Light chain                           | MW     |
|-----------|---------------------------------------|--------|
| CT2.1.3   | ND                                    | ND     |
| CT3.1.1   | NH2-DIQMTQSPSSLSASVGDRVT              | 26,119 |
| CT4.1.1   | NH2-EIVLTQSPGTLSLSPGERAT              | 23,917 |
| CT4.8.1   | NH2-EIVLTQSPGTLSLSPGERAT              | 23,617 |
| CT4.9.1   | NH2-DIQMTQSPSSVSASVGDRVT              | 23,702 |
| CT4.10.2  | NH2-TGEFVLTQSPGTLSLSPGER (60%)        | 24,101 |
|           | NH2-EFVLTQSPGTLSLSPGERAT (40%)        |        |
| CT4.14.3  | NH2-EIVLTQSPGTLSLSPGERAT              | 23,770 |
| CT4.13.1  | NH <sub>2</sub> -EIVLTQSPGTLSLSPGERAT | 23,802 |
| CT6.1.1   | NH2-EIVLTQSPGTLSLSPGERAT              | 23,747 |

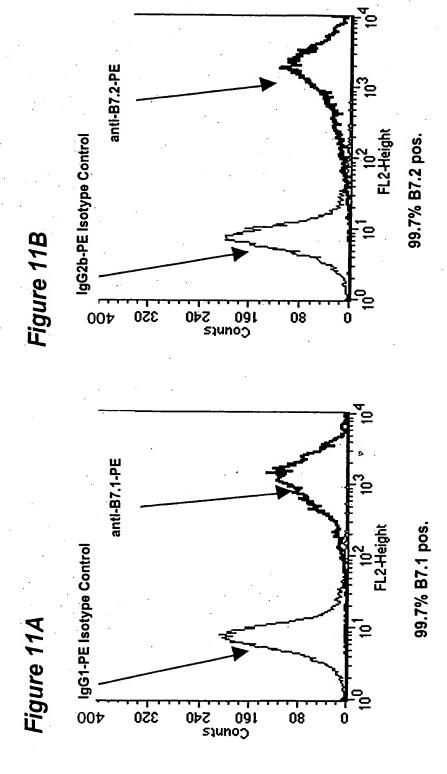
| Heavy chain   | MW   |
|---|--|
| ND  | ND   |
| NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase:              | 51,813   |
| NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~80%)                   | ,  |
| NH <sub>2</sub> -PEVQF(minor sequence-20%)                                      |  |
| NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase:              | 51,502   |
| NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~65%)                   |  |
| NH <sub>2</sub> -PEVQFNWYVD(minor sequence~35%)                                 |  |
| NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase:              | 51,597   |
| NH <sub>2</sub> -pQ-VQLVESGGGVVQPG(R)SL (major sequence~60%)                    |  |
| NH <sub>2</sub> -PEVQFNWY(minor sequence-40%)                                   |  |
| NH <sub>2</sub> -EVQLLESGGGLVQPGGSLRL (free amino terminus)                     | 51,437   |
| NH <sub>2</sub> -Blocked. Following treatment with Pyroglutmate Aminopeptidase: | 51,502   |
| NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence-60%)                   |  |
| NH <sub>2</sub> -PEVQFNWYVD(minor sequence-40%)                                 |  |
| NH <sub>2</sub> -Blocked. Following treatment with Pyroglutmate Aminopeptidase: | 51,293   |
| NH2-pQ-VQLVESGGGVVQPGRSL(R)(L)(S) (major sequence-65%)                          |  |
| NH <sub>2</sub> -PEVQFNWYV(minor sequence~35%)                                  |  |
| NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase:              | 51,305   |
| NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~75%)                   |  |
| NH <sub>2</sub> -PEVQFN(minor sequence~25%)                                     |  |
| NH <sub>2</sub> -Blocked. Following treatment with Pyroglutmate Aminopeptidase: | 51,476   |
| <del>_</del> -  |  |
|   |  |
|   | ND  NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase: NH2-pQ-VQLVESGGGVVQPGRSLRLS (major sequence-80%) NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase: NH2-pQ-VQLVESGGGVVQPGRSLRLS (major sequence-65%) NH2-PEVQFNWYVD(minor sequence-35%) NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase: NH2-pQ-VQLVESGGGVVQPG(R)SL (major sequence-60%) NH2-PEVQFNWY (minor sequence-40%) NH2-PEVQFNWY (minor sequence-40%) NH2-EVQLLESGGGLVQPGGSLRL (free amino terminus) NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase: NH2-pQ-VQLVESGGGVVQPGRSLRLS (major sequence-60%) NH2-PEVQFNWYVD (minor sequence-40%) NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase: NH2-pQ-VQLVESGGGVVQPGRSL(R)(L)(S) (major sequence-65%) NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase: NH2-PQ-VQLVESGGGVVQPGRSLRLS (major sequence-75%) NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase: NH2-pQ-VQLVESGGGVVQPGRSLRLS (major sequence-75%) NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase: NH2-PQ-VQLVESGGGVVQPGRSLRLS (major sequence-65%) NH2-Blocked. Following treatment with Pyroglutmate Aminopeptidase: NH2-PQ-VQLVESGGGVVQPGRSLRLS (major sequence-65%) |

<sup>\*</sup> This heavy chain sequence is similar to the other blocked heavy chain sequences except for a unique Gln->Glu change at position 13.

|                         | Conc. (mg/r   | Conc. (mg/ml) (Ec1.58)  | IEF           | SDS-PAGE  | GE       | SEC      | reported MALDI | MALDI  | n-term. s                       | n-term. seq. (lc)*              |
|-------------------------|---|---|---------------|---|----------|----------|----------------|--------|---------------------------------|---------------------------------|
| antibody                | reported  | observed  | observed      | (+) b-me  | (-) b-me | observed | Hc             | тс     | reported                        | observed                        |
| CT 3.1.1                | 11  | 1.57  | smear         | 50 & 28 kDa   | 6 bands  | 139,400  | 51,813         | 26,119 | DIQMTQSP<br>(SEQ ID NO:<br>141) | DIQMTQSP<br>(SEQ ID NO:<br>141) |
| CT 4.1.1                | 1.54  | 1.65  | smear         | 50 & 24 kDa   | 6 bands  | 79,900   | 51,502         | 23,917 | EIVLTQSP (SEQ<br>ID NO: 142)    | EIVLTQSP (SEQ<br>ID NO: 142)    |
| CT 4.8.1                | 1.52  | 1.54  | 4 bands       | 50 & 24 kDa   | 6 bands  | 110,300  | 51,597         | 23,617 | EIVLTQSP (SEQ<br>ID NO: 143)    | EIVLTQSP (SEQ<br>ID NO: 143)    |
| CT 4.10.2               | 1.29  | 1.77  | 4 bands       | 50 & 25 kDa   | 6 bands  | 107,200  | 51,502         | 24,101 | **                              | ***                             |
| CT 4.14.3               | 1.75  | 1.65  | smear         | 50 & 24 kDa   | 6 bands  | 82,800   | 51,293         | 23,770 | EIVLTQSP<br>(SEQ ID NO:<br>146) | EIVLTQSP (SEQ<br>ID NO: 146)    |
| CT 6.1.1                | 1.36  | 1.3   | 4 bands       | 50 & 24 kDa   | 6 bands  | 101,100  | 51,476         | 23,747 | EIVLTQSP (SEQ<br>ID NO: 147)    | EIVLTQSP (SEQ<br>ID NO: 147)    |
| * all heavy             | chains n-termi  | all heavy chains n-terminally blocked (not sequenced in-house)                | (not sequenc  | ed in-house)  |          |          |                |        |                                 |                                 |
| ** mixed se<br>EFVLTQSP | ** mixed sequence reported: TGEF\<br>EFVLTQSP (40) (SEQ ID NO: 145) | ** mixed sequence reported: TGEFVLTQSP (60)<br>EFVLTQSP (40) (SEQ ID NO: 145) | _             | (SEQ ID NO: 144) &  | <i>જ</i> |          |                |        |                                 |                                 |
| *** mixed s<br>EFVLTQSP | *** mixed sequence observed TGEF<br>EFVLTQSP (40) (SEQ ID NO: 145)  | ved TGEFVL7<br>NO: 145)   | rqsp (60) (\$ | *** mixed sequence observed TGEFVLTQSP (60) (SEQ ID NO: 144) & EFVLTQSP (40) (SEQ ID NO: 145) | % (t     |          | <b>E</b>       |        |                                 | *                               |

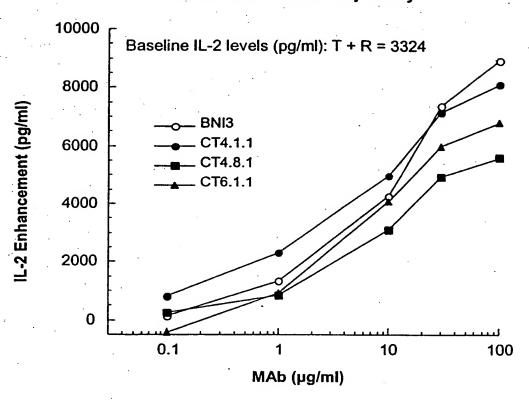
IOD<sub>280nm</sub>=0.633 mg/ml Ec-1.58





Expression of B7.1 and B7.2 on Raji Cells

# Enhancement of Human T Cell IL-2 Production Induced by Anti-CTLA4 XenoMouse MAbs in the 72 Hour T Blast / Raji Assay



Enhancement of Human T Cell IFN-γ Production Induced by Anti-CTLA4 XenoMouse MAbs in the 72 Hour T Blast / Raji Assay

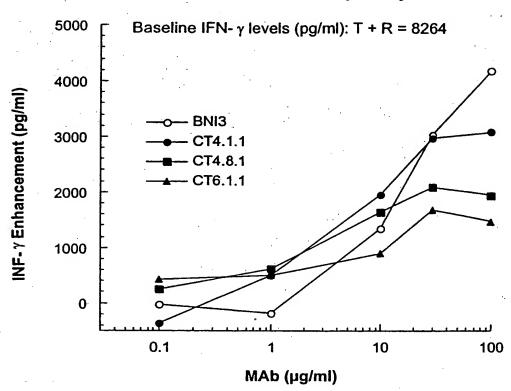
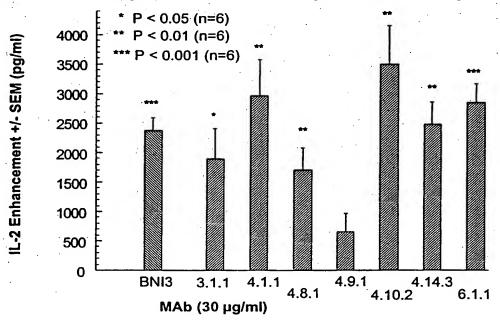


Figure 14

Enhancement of Human T Cell IL-2 Production Induced by Anti-CTLA4 XenoMouse MAbs in the 72 Hour T Blast / Raji Assay (6 Donors)

Baseline IL-2 levels (pg/ml): T + R = 9187, T + R + IgG2a = 9389, T + R + IgG2 = 8509



Enhancement of Human T Cell IFN- γ Production Induced by Anti-CTLA4 XenoMouse MAbs in the 72 Hour T Blast / Raji Assay (6 Donors)

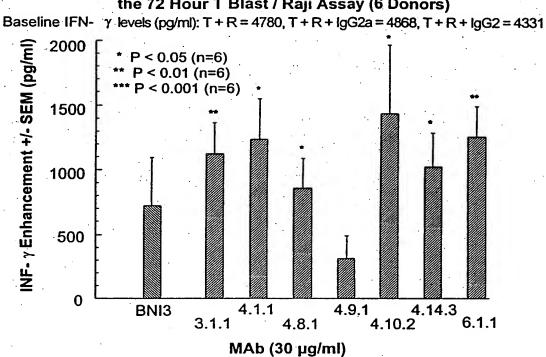


Figure 16

Enhancement of IL-2 Production Induced by Anti-CTLA4 MAb CT4.1.1 (30  $\mu$ g/ml) Binding to Human PBMC Stimulated with SEA (100 ng/ml) Plus Anti-CD3 MAb (60 ng/ml)

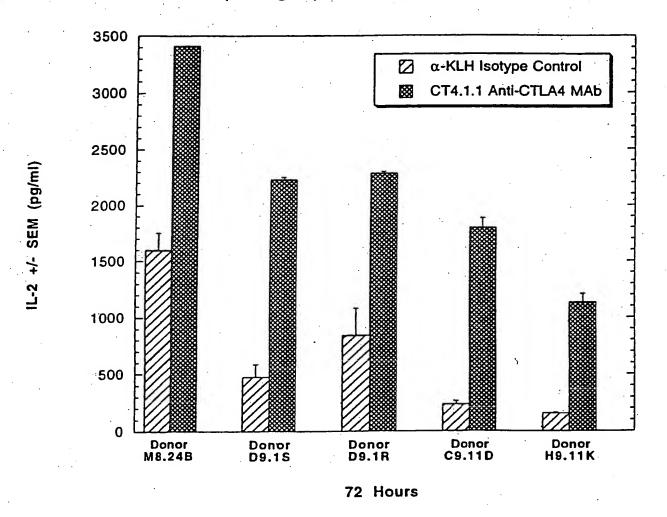
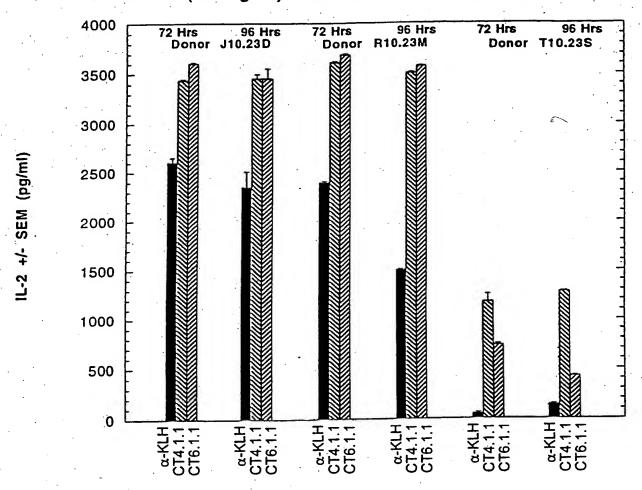
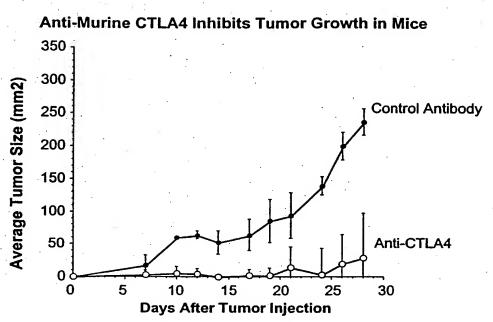


Figure 17

Enhancement of IL-2 Production Induced by Anti-CTLA4 MAbs (30 μg/ml) in Human Whole Blood Stimulated with SEA (100 ng/ml) Plus Anti-CD3 MAb (60 ng/ml)



# Figure 18



Treatment was administered on day 0,4,7,and 14 after tumor challenge

Figure 19

Enhancement of IL-2 Production Induced by Anti-CTLA4 MAbs (30 μg/ml) in the 72 Hour T Blast / Raji and Superantigen Assays (6 Donors)

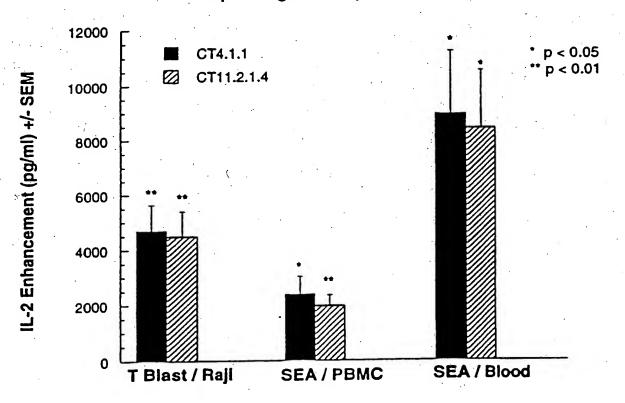


Figure 20

# Enhancement of Human T Cell IL-2 Production Induced by Anti-CTLA4 MAbs in the 72 Hour T Blast / Raji Assay

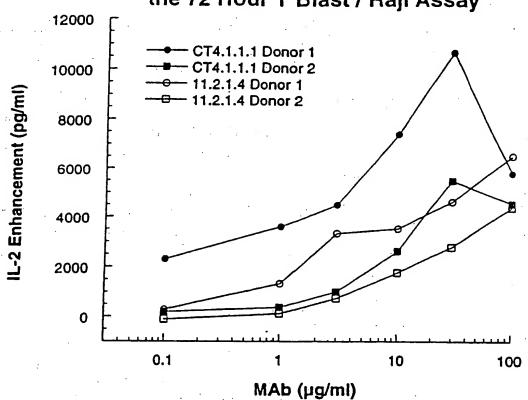
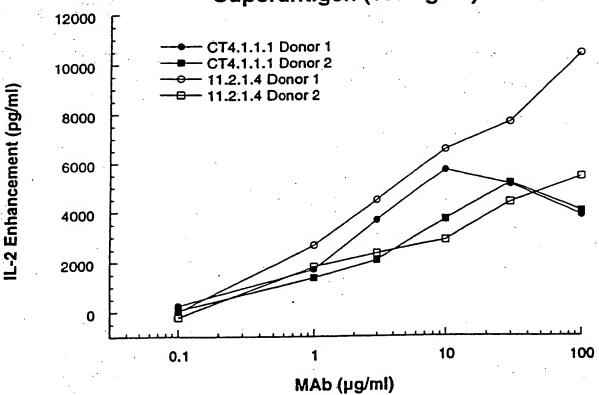


Figure 21

# Enhancement of IL-2 Production Induced by Anti-CTLA4 MAbs in Whole Blood Stimulated with Superantigen (100 ng/ml)



- · Signal peptides shown in bold and large text
- Open reading frame for genomic clone underlined
- Mutations introduced to make deglycosylated Ab (N294Q) double underlined and large text

# Figure 22A 4.1.1 IgG2 Heavy Chain cDNA

### ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTAAGA

**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTCACCTTCAGTAG CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT TCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC CGAGAGCACAGCGGCCTGGGCTGGTCAAGGACTACTTCCCCGAACCGG TGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGCCCA CCGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAA TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCAC GTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAA ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC AAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG GAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:53)

# Figure 22B 4.1.1 IgG2 Heavy Chain Genomic DNA

### ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTAAGA

**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTCACCTTCAGTAG CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA <u>CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT</u>  ${f TCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCT}$ AGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC CGAGAGCACAGCGGCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG TGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA <u>GCTGTCCTACAGTCCTCAGGACTCTACTCCCT</u>CAGCAGCGTGGTGACCGTGCC CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA GTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTG CAGCCCCAGCCCAGGGCAGCAAGGCCCCATCTGTCTCCTCACCCGGAGG CCTCTGCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC GGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGC CCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGAC ACCTTCTCTCCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGC CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGG CCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTCCTCAGCACCACCTGT GGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGAC <u>CCCGAGGTCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAA</u> <u>GACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCC</u> <u>TCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTC</u> TCCAACAAAGGCC<u>TCCCAGCCCCCATCGAG</u>AAAACCATCTCCAAAACCAAAGG TGGGACCCGCGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCC TCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCG AGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACC <u>AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG</u> <u>GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCAT</u> GCTGGACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA GCAGGTGCCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTG CACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:54)

# Figure 22C 4.1.1 IgG2 Heavy Chain Protein

MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCVASGFTFSS
HGMHWVRQAPGKGLEWVAVIWYDGRNKYYADSVKGRFTISRDNSKNTLFLQMN
SLRAEDTAVYYCARGGHFGPFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTS
ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST
FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO:63)

# Figure 22D 4.1.1 IgG2 Heavy Chain cDNA N294Q

ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTAAGA **GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTCACCTTCAGTAG CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT TCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC CGAGAGCACAGCGGCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG TGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGCCCA CCGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAA TGGACGTGAGCCACGAGACCCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCCAAAGCAC GTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAA ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC AAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG GAGAACAACTACAAGACCACCTCCCATGCTGGACTCCGACGGCTCCTTCTT CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:55)

# Figure 22E 4.1.1 IgG2 Heavy Chain Protein N2940

MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCVASGFTFSS
HGMHWVRQAPGKGLEWVAVIWYDGRNKYYADSVKGRFTISRDNSKNTLFLQMN
SLRAEDTAVYYCARGGHFGPFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTS
ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFQST
FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO:64)

# Figure 22F 4.1.1 Kappa Chain DNA

## **ATGGAAACCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC**

CCAGATACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC
TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTATTA
GCAGCAGCTTCTTAGCCTGGTACCAGCAGAGACCTGGCCAGGCTCCCAGGCTC
CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGG
CAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAG
ATTTTGCAGTGTATTACTGTCAGCAGTATGGTACCTCACCCTGGACGTTCGGC
CAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCC
TGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAC
GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGCAGCAAGGA
CAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCCTCGCCCGTC

# Figure 22G 4.1.1 Kappa Chain Protein

ACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:56)

METPAQLLFLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSIS SSFLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYGTSPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK HKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:65)

# Figure 22H 4.8.1 Heavy Chain DNA

### **ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTAAGA**

**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG CCTGGGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTCACCTTCAGTAA CAGTTATATGGTATGATGGAAGTAATAAACACTATGGAGACTCCGTGAAGGGC CGATTCACCATCTCCAGTGACAATTCCAAGAACACGCTGTATCTGCAAATGAA TGGGGTCCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCAC CGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTC CCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC CCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGC CCACCGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTTCCCCCC TGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAG CACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAG AAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT TCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG CCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTT CTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG AGCCTCTCCCTGTCTCCGGGTAAATGA (SEO ID NO:57)

# Figure 221 4.8.1 Heavy Chain Protein

MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCTASGFTFSN YGMHWVRQAPGKGLEWVAVIWYDGSNKHYGDSVKGRFTISSDNSKNTLYLQMN SLRAEDTAVYYCARGERLGSYFDYWGQGTLVTVSSASTKGPSVFPLAPCSRST SESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:66)

# Figure 22J 4.8.1 Kappa Chain DNA

## ATGGAAACCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC

CCAGATACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC
TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGACCAGTGTTAGCAGCA
GTTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTATC
TATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGG
GTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTG
CAGTCTATTACTGTCAGCAGTATGGCATCTCACCCTTCACTTTCGGCGGAGGG
ACCAAGGTGGAGATCAAGCGAACTGTGGCTGCACCATCTGTCTTCATCTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA
ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTC
CAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAC
CTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACA
AAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
AGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:58)

# Figure 22K 4.8.1 Kappa Chain Protein

METPAQLLFLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRTSVSSS YLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGISPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:67)

# Figure 22L 6.1.1 Heavy Chain DNA

### ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTAAGA

**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAG CCTGGGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTCACCTTCAGTAG CAGTTATATGGTATGATGGAAGCAATAAACACTATGCAGACTCCGCGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGACTGC TGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC CGAGAGCACAGCGGCCCTGGGCTGCTGAAGGACTACTTCCCCGAACCGG TGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTCGAGTGCCCA CCGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAA TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCAC GTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAA ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC AAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG GAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:59)

# Figure 22M 6.1.1 Heavy Chain Protein

MEFGLSWVFLVALLRGVQCQVQLVESGGGVVEPGRSLRLSCTASGFTFSS YGMHWVRQAPGKGLEWVAVIWYDGSNKHYADSAKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARAGLLGYFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:68)

# Figure 22N 6.1.1 Kappa Chain DNA

## ATGGAAACCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC

CCAGATACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC
TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGTAGGGCCAGTCAAAGTGTTA
GCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCCCCTC
ATCTATGGTGTATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAG
TGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATT
TTGCAGTGTATTACTGTCAGCAGTATGGTATCTCACCATTCACTTTCGGCCCT
GGGACCAAAGTGGATATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTT
CCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGC
TGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC
CTCCAATCGGGTAACTCCCAGGAGAGTTCACAGAGCAGGACAGCAAGGACAG
CACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCCAGACTACGAGAAAC
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA
AAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:60)

# Figure 220 6.1.1 Kappa Chain Protein

METPAQLLFLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVS SYLAWYQQKPGQAPRPLIYGVSSRATGIPDRFSGSGSGTDFTLTISRLEPEDF AVYYCQQYGISPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:69)

# Figure 22P 11.2.1 IgG2 Heavy Chain DNA:

ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTAAGA **GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG CCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAG CAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGAGGG GAGCTACCCTTTACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACC ACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC GCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACC AGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCT CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCT GCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGC AAATGTTGTGTCGAGTGCCCACCGTGCCCAGCACCACCTGTGGCAGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCC CTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAG TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG GGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGC ACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGC CTCCCAGCCCCATCGAGAAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGA ACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGG TCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCT GGACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:61)

# Figure 22Q 11.2.1 IgG2 Heavy Chain Protein:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDPRGATLY YYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDH KPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:70)

# Figure 22R 11.2.1 IgG2 Kappa Chain DNA:

## ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTC

TGGCTCCGAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCCT
CCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAG
AGCATTAACAGCTATTTAGATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA
ACTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA
GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCAACTTACTACTGTCAACAGTATTACAGTACTCCATTCACTTT
CGGCCCTGGGACCAAAGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCT
TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG
TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGA
TAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGCACAGCA
AGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTAC
GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCCATCAGGGCCTGAGCTCGCC
CGTCACAAAGACTTCAACAGGGGAAGTGTTAGTGA (SEQ ID NO:62)

# Figure 22S 11.2.1 IgG2 Kappa Chain Protein:

DIQMTQSPSSLSASVGDRVTITCRASQSINSYLDWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPFTFGPGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC (SEQ ID NO:71)